

24350

SEARCH REQUEST FORM

Requestor's

Name:

GAMBEL

Serial

Number:

08/487283

Date:

9/6/00

Phone:

303-3997

Art Unit:

1644

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

9/6-9/6/00-

SEQ + SEQ INTERFERENCE SEARCH

abn 9/6-494-458

9/7-431-435

343-394

9/9-350-354

9/10-297-301

9/11-250-254

9/12-195-199

(25-29)

SEQ 10 NO: 1

NO: 12

SEQ 10 NO: 8

(+ CLOSURE)

AAS-12 of SEQ 10 NO: 1

①

lys Ser Ser lys Cys

②

REQUEST
JAN

STAFF USE ONLY

Date completed:

9/13/00

Searcher:

Jan

Terminal time:

40

Elapsed time:

CPU time:

+ 10/

Total time:

Number of Searches:

2

Number of Databases:

Search Site

STIC

CM-1

Pre-S

Type of Search

24 N.A. Sequence

3 A.A. Sequence

Structure

Bibliographic

Vendors

IG

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other

=> fil reg

FILE 'REGISTRY' ENTERED AT 07:04:18 ON 13 SEP 2000
 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
 PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
 COPYRIGHT (C) 2000 American Chemical Society (ACS)

STRUCTURE FILE UPDATES: 12 SEP 2000 HIGHEST RN 288839-14-5
 DICTIONARY FILE UPDATES: 12 SEP 2000 HIGHEST RN 288839-14-5

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 11, 2000

Please note that search-term pricing does apply when
 conducting SmartSELECT searches.

Structure search limits have been increased. See HELP SLIMIT
 for details.

=> e ksskc/sqep

E1	1	KSSKAVAAWTLKAAAAGPSNTPPEI/SQEP
E2	1	KSSKAVAAWTLKAAAVNIRNCCYI/SQEP
E3	0 -->	KSSKC/SQEP
E4	1	KSSKESSKKPKENKPLKEEKIVPKMAFKEPKPMSKEPKPDSNLLTITSGQDKKAPSKRPP ISDSEELSAKKRKKSSSEALFKSFSSAPPLILTCSADKKQIKDKSHVKGKVKIESETSE KKKSTLPPFDDIVDPNDSVEENISSKSDSEQSPASSSSSSSSSFTPSQTRQQGPLRSI MKDLHSDDNEEESDEVEDND/SQEP
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E6	1	KSSKHRSFLLKKSGGNQVSLYQKWWNSQLKKSLCYSTVAALI FMIP SQESFADSLIDLNL GLDPSVECLSGDGAFSVGYFTKAGSTPVEYQPFKYDVS KKTFTILSVETANQSGYAYGIS YDGTITVGTCSLGAGKYNGAKWSADGTLTPLTGITGGTSHTEARAISKDTQVIEGFSYDA SGQPKAVQWASGGLQ/SQEP
E7	1	KSSKKPRKRKTTHKRK/SQEP
E8	1	KSSKLVSANRLFG/SQEP
E9	1	KSSKSPSKKKKKKPGDC/SQEP
E10	2	KSSL/SQEP
E11	1	KSSLEDQKIKEKLQPAEIETCMKTITITILEWLEKNQLAGKDEYEAKNKEAESVCAPIMSK IYQD/SQEP
E12	1	KSSLEEPDFYKTKIK/SQEP

=> d his

(FILE 'HOME' ENTERED AT 06:58:21 ON 13 SEP 2000)
 SET COST OFF

FILE 'REGISTRY' ENTERED AT 06:58:25 ON 13 SEP 2000
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 E VIDHQGTKSSKCVRQKVEGSS/SQEP

L1 1 S E3

FILE 'HCAOLD' ENTERED AT 06:59:13 ON 13 SEP 2000
 0 S L1

FILE 'HCAPLUS' ENTERED AT 06:59:15 ON 13 SEP 2000
 L3 1 S L1
 SEL RN

FILE 'REGISTRY' ENTERED AT 06:59:40 ON 13 SEP 2000
 L4 32 S E1-E32
 L5 14 S L4 AND PROTEIN/FS
 L6 18 S L4 NOT L5
 L7 17 S L6 AND NUCLEIC/FS

Point of Contact:
 Jan Delaval
 Librarian-Physical Sciences
 CM1 1E01 Tel: 308-4498

L8 3 S L7 AND 747/SQL
L9 4 S L7 AND 750/SQL

FILE 'HCAOLD' ENTERED AT 07:01:28 ON 13 SEP 2000
L10 0 S L8 OR L9

FILE 'HCAPLUS' ENTERED AT 07:01:31 ON 13 SEP 2000
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L12 1 S L3,L11
L13 0 S LYS SER SER LYS CYS
L14 1 S KSSKC
L15 1 S L12,L14

FILE 'USPATFULL' ENTERED AT 07:02:36 ON 13 SEP 2000
L16 1 S L1 OR L8 OR L9
L17 0 S KSSKC

FILE 'HCAPLUS, USPATFULL' ENTERED AT 07:04:02 ON 13 SEP 2000
L18 2 DUP REM L15 L16 (0 DUPLICATES REMOVED)

FILE 'REGISTRY' ENTERED AT 07:04:18 ON 13 SEP 2000
E KSSKC/SQEP

=> d sqide can l1

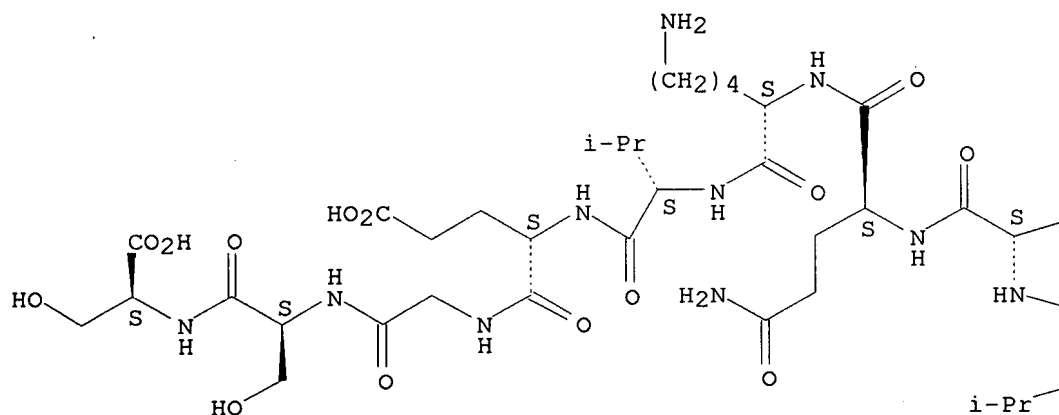
L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2000 ACS
RN 172998-82-2 REGISTRY
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FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 21

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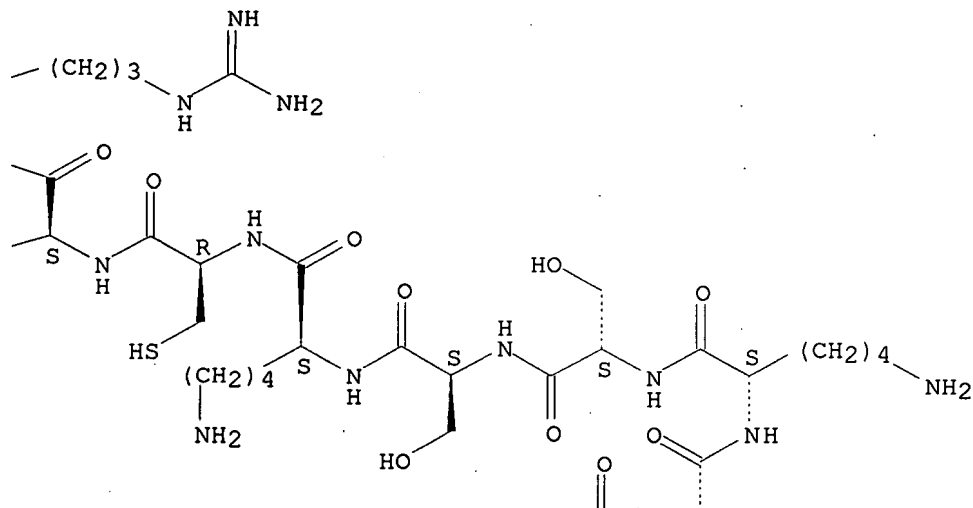
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SR CA
LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

Absolute stereochemistry.

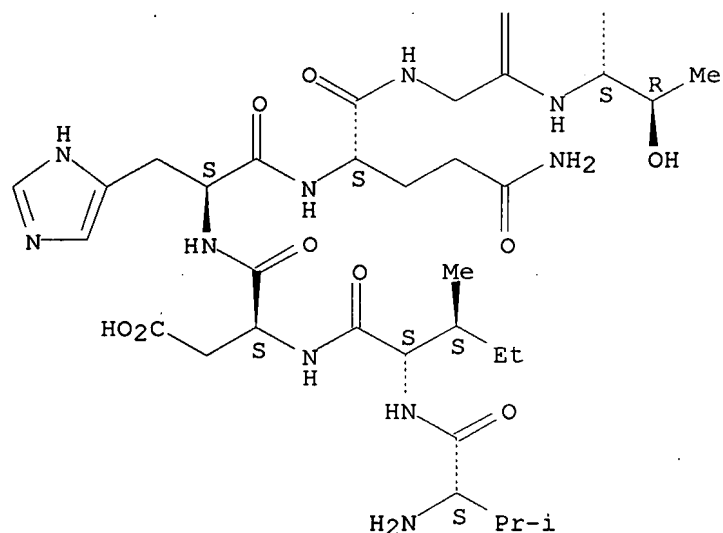
PAGE 1-A



PAGE 1-B



PAGE 2-B



1 REFERENCES IN FILE CA (1967 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

=> d sqide can 18 tot

L8 ANSWER 1 OF 3 REGISTRY COPYRIGHT 2000 ACS

RN 173012-28-7 REGISTRY

CN DNA (human-mouse clone 5G1.1 scFv DO12 immunoglobulin G1 anti-antigen CD 5-specifying) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human-mouse clone 5G1.1 scFv DO12 immunoglobulin G1 anti-antigen CD 5-specifying)
FS NUCLEIC ACID SEQUENCE
SQL 747
NA 159 a 189 c 211 g 188 t
NTE doublestranded

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       251 acttcgctac gtattactgt cagaacgttt taaatactcc gttgactttc
       301 ggacagggta ccaagggtga aataaaacgt actggcgggtg gtggttctgg
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       501 cgggcagggc ctggaatgga tgggtgagat cttaccgggc tctggtagca
       551 ccgaatatgc caaaaattc cagggccgtg ttactatgac gcgtgacact
       601 tcgactagta cagtatacat ggagctctcc agcctgcgat cggaggacac
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MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

L8 ANSWER 2 OF 3 REGISTRY COPYRIGHT 2000 ACS

RN 173012-11-8 REGISTRY

CN DNA (human-mouse clone 5G1.1 scFv immunoglobulin G1 anti-antigen CD 5-specifying) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human-mouse clone 5G1.1 scFv immunoglobulin G1 anti-antigen CD 5-specifying)

FS NUCLEIC ACID SEQUENCE

SQL 747

NA 161 a 186 c 209 g 191 t

NTE doublestranded

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MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

L8 ANSWER 3 OF 3 REGISTRY COPYRIGHT 2000 ACS
 RN 173012-09-4 REGISTRY
 CN DNA (mouse clone 5G1.1M1 scFv immunoglobulin G1 anti-antigen CD 5-specifying cDNA) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (mouse clone 5G1.1M1 scFv immunoglobulin G1 anti-antigen CD 5-specifying messenger RNA-complementary)

FS NUCLEIC ACID SEQUENCE

SQL 747

NA 183 a 174 c 211 g 179 t

NTE doublestranded

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     151 tatggtgcaa ccaacttggc agatggcatg tcatcgaggt tcagtggcag
     201 tggatctggt agacagtatt atctcaagat cagtagcctg catcctgacg
     251 atgttgcaac gtattactgt caaaatgtgt taaatactcc tctcacgttc
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MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL
 1 REFERENCES IN FILE CA (1967 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

=> d sqide can 19 tot

L9 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2000 ACS
 RN 173012-26-5 REGISTRY
 CN DNA (human-mouse clone 5G1.1VH+IGHRLD immunoglobulin G1 anti-antigen CD 5-specifying) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human-mouse clone 5G1.1VH+IGHRLD immunoglobulin G1 anti-antigen CD 5-specifying)

FS NUCLEIC ACID SEQUENCE

SQL 750

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NTE doublestranded

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MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

L9 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2000 ACS
RN 173012-18-5 REGISTRY
CN DNA (human-mouse clone 5G1.1 VH + IGHRLC immunoglobulin G1 anti-antigen CD 5-specifying cDNA) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (human-mouse clone 5G1.1 VH + IGHRLC immunoglobulin G1 anti-antigen CD 5-specifying messenger RNA-complementary)
FS NUCLEIC ACID SEQUENCE
SQL 750
NA 163 a 220 c 197 g 170 t
NTE doublestranded

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MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

L9 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2000 ACS
RN 173012-16-3 REGISTRY
CN DNA (human-mouse clone 5G1.1VH+IGHRL immunoglobulin G1 anti-antigen CD 5-specifying) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (human-mouse clone 5G1.1VH+IGHRL immunoglobulin G1 anti-antigen CD 5-specifying)
FS NUCLEIC ACID SEQUENCE
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NTE doublestranded

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CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

L9 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2000 ACS

RN 173012-15-2 REGISTRY

CN DNA (human-mouse clone 5G1.1M1 VH +HuG1 immunoglobulin G1 anti-antigen CD 5-specifying) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human-mouse clone 5G1.1M1 VH +HuG1 immunoglobulin G1 anti-antigen CD 5-specifying)

FS NUCLEIC ACID SEQUENCE

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NTE doublestranded

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MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

=> fil hcaplus uspatful

FILE 'HCAPLUS' ENTERED AT 07:04:53 ON 13 SEP 2000

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FILE 'USPATFULL' ENTERED AT 07:04:53 ON 13 SEP 2000

CA INDEXING COPYRIGHT (C) 2000 AMERICAN CHEMICAL SOCIETY (ACS)

=> d bib abs hitrn tot

L18 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2000 ACS

AN 1996:73261 HCAPLUS

DN 124:127101

TI Anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases

IN Evans, Mark J.; Matis, Louis; Mueller, Eileen Elliott; Nye, Steven H.; Rollins, Scott; Rother, Russell P.; Springhorn, Jeremy P.; Squinto, Stephen P.; Thomas, Thomas C.; et al.

PA Alexion Pharmaceuticals, Inc., USA

SO PCT Int. Appl., 159 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9529697	A1	19951109	WO 1995-US5688	19950501
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	RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	US 6074642	A	20000613	US 1994-236208	19940502
	CA 2189015	AA	19951109	CA 1995-2189015	19950501
	AU 9524747	A1	19951129	AU 1995-24747	19950501
	EP 758904	A1	19970226	EP 1995-919041	19950501
	R: AT, BE, CH, DE, DK, ES, FR, GB, IE, IT, LI, NL, PT, SE				
	BR 9507594	A	19970916	BR 1995-7594	19950501
	JP 10500289	T2	19980113	JP 1995-528523	19950501
PRAI	US 1994-236208		19940502		
	WO 1995-US5688		19950501		
AB	The use of anti-C5 antibodies, e.g., monoclonal antibodies, to treat glomerulonephritis (GN) is disclosed. The administration of such antibodies at low dosage levels has been found to significantly reduce glomerular inflammation/enlargement and other pathol. conditions assocd. with GN. Also disclosed are novel anti-C5 antibodies and anti-C5 antibody-encoding nucleic acid mols. These antibodies are useful in the treatment of GN and other inflammatory conditions involving pathol. activation of the complement system.				
IT	172998-82-2P				
	RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses) (epitope KSSKC -contg. antigen; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)				
IT	173012-09-4P 173012-11-8P 173012-15-2P 173012-16-3P 173012-18-5P 173012-26-5P 173012-28-7P				
	RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses) (nucleic acid sequence; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)				

L18 ANSWER 2 OF 2 USPATFULL

AN 2000:73908 USPATFULL

TI Use of antibodies specific to human complement component C5 for the treatment of glomerulonephritis

IN Wang, Yi, Orange, CT, United States

Matis, Louis, Southport, CT, United States

Rollins, Scott, Monroe, CT, United States

PA Alexion Pharmaceuticals, Inc., New Haven, CT, United States (U.S. corporation)

PI US 6074642 20000613
AI US 1994-236208 19940502 (8)
DT Utility
EXNAM Primary Examiner: Feisse, Lila; Assistant Examiner: Gambel, Phillip
LREP Fidel, Seth A.; Klee, Maurice M.
CLMN Number of Claims: 5
ECL Exemplary Claim: 1
DRWN 14 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 1197

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The use of anti-C5 antibodies, e.g., monoclonal antibodies, to treat glomerulonephritis (GN) is disclosed. The administration of such antibodies at low dosage levels has been found to significantly reduce glomerular inflammation/enlargement and other pathologic conditions associated with GN.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT **172998-82-2P**
(epitope KSSKC-contg. antigen; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT **173012-09-4P 173012-11-8P 173012-15-2P**
173012-16-3P 173012-18-5P 173012-26-5P
173012-28-7P
(nucleic acid sequence; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

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MSPrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:22:05 2000; Maspar time 4.08 Seconds

Tabular output not generated. 57.866 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (8-12) from US08487283A.pep
Perfect Score: 35
Sequence: 1 KSSKC 5

Scoring table:
PAM 150
Gap 15

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 5

Database: pIr64
1:PIr1 2:PIr2 3:PIr3 4:PIr4

Statistics: Mean 16.465; Variance 17.344; scale 0.949

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	ID	Description	Pred. No.

No matches found.

Search completed: Wed Sep 6 08:23:04 2000
Job time : 59 secs.

M P E R C H
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Mserch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:19:32 2000; MasPar time 2.56 Seconds

Tabular output not generated. 60.533 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (8-12) from US08487283A.pep
Perfect Score: 35
Sequence: 1 KSSKC 5

Scoring table: PAM 150
Gap 15

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 5

Database: swiss-prot38
1:swissprot

Statistics: Mean 16.989; Variance 16.059; scale 1.058

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match length	ID	Description	Pred. No.

No matches found.

Search completed: Wed Sep 6 08:20:17 2000
Job time : 45 secs.

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Msrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:20:34 2000; Maspar time 5.75 Seconds

Tabular output not generated. 60.308 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (8-12) From US08487283A.pep
Perfect Score: 35
Sequence: 1 KSSKC 5

Scoring table: PAM 150
Gap 15

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 5

Database: sptrembl12
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_protein 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 16.549; Variance 15.598; scale 1.061

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match length	ID	Description	Pred. No.

No matches found.

Search completed: Wed Sep 6 08:21:48 2000
Job time : 74 secs.

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MPerch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:23:22 2000; MasPar time 2.62 Seconds

Tabular output not generated. 45.269 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (8-12) from US08487283A.pep
Perfect Score: 35
Sequence: 1 KSKC 5

Scoring table: PAM 150
Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 5

Database: a-geneseq36
1:geneseqp

Statistics: Mean 12.105; Variance 34.177; scale 0.354

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	ID	Description	Pred. No.

No matches found.

Search completed: Wed Sep 6 08:24:11 2000
Job time : 49 secs.

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:25:39 2000; Maspar time 12.13 Seconds

Tabular output not generated. 50.906 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (8-12) from US08487283A.pep
Perfect Score: 35
Sequence: 1 KSSRC 5

Scoring table: PAM 150
Gap 15

Searched: 820620 seqs, 123522873 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 5

Database: a-pending
1:PCN 2:U6 3:U60 4:U7 5:U80 6:U81 7:U82 8:U83 9:U84A
10:U84B 11:U85 12:U86 13:U87 14:U88 15:U89 16:U90 17:U91
18:U92 19:U93 20:U94 21:U95 22:NEWP 23:NEWU60 24:NEWU7
25:NEWU8 26:NEWU9

Statistics: Mean 13.804; Variance 29.044; scale 0.475

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.

No matches found.

Search completed: Wed Sep 6 08:27:12 2000
Job time : 93 secs.

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Mperch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:24:29 2000; MasPar time 2.21 Seconds

Tabular output not generated. 34.699 Million cell updates/sec

Title: >US-08-487-283A-1

Description: (8-12) from US08487283A.pep

Perfect Score: 35

Sequence: 1 KSSKC 5

Scoring table: PAM 150
Gap 15

Searched: 152433 seqs, 15329240 residues

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Maximum DB seq length 5

Database: a-issued

1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 11.504; Variance 33.907; scale 0.339

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.

No matches found.

Search completed: Wed Sep 6 08:25:20 2000
Job time : 51 secs.

 M P S E R H
 ***** (TM)

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Msrch:pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Wed Sep 6 08:16:42 2000; MasPar time 4.45 seconds
 Tabular output not generated. 222.630 Million cell updates/sec

Title: >US-08-487-283A-1
 Description: (1-21) from US08487283A.pep
 Perfect Score: 141
 Sequence: 1 VIDHOGTKSSKCVRKVEGSS 21

Scoring table: PAM 150
 Gap 15

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: pir64
 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 25.757; Variance 31.889; scale 0.808

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	141	100.0	1676	1 C5HU	complement C5 precurs	2.35e-22
2	69	48.9	1680	1 C5MS	complement C5 precurs	3.83e-03
3	68	48.2	936	2 H71862	probable cytochrome C	6.49e-03
4	65	46.1	936	2 B64567	cytochrome c biogenesis	3.07e-02
5	63	44.7	213	2 T10422	MADS box protein A -	8.46e-02
6	62	44.0	213	2 S76070	hypothetical protein	1.39e-01
7	61	43.3	214	2 T00879	MADS box protein AGT2	2.29e-01
8	60	42.6	1166	2 H71609	hypothetical protein	3.74e-01
9	59	41.8	940	2 S49087	lactoferrin binding p	6.08e-01
10	58	41.1	1002	2 A56678	yeamanulein-alpha - f	9.82e-01
11	58	41.1	164	2 A65068	hypothetical protein	9.82e-01
12	58	41.1	205	2 T49364	protein tyrosine phos	9.82e-01
13	58	41.1	223	2 T49365	protein tyrosine phos	9.82e-01
14	58	41.1	259	2 F70677	hypothetical protein	9.82e-01
15	57	40.4	117	2 T68524	ribosomal protein L34	1.58e+00
16	57	40.4	264	2 S28969	N-carbamoylsarcosine	1.58e+00
17	56	39.7	236	2 T01662	globulin-1 - maize (f	2.52e+00
18	56	39.7	407	2 T02258	globulin-1 - maize	2.52e+00
19	56	39.7	537	2 B33485	spore coat protein SP	2.52e+00
20	56	39.7	543	2 S21825	vicillin-like storage	2.52e+00
21	55	39.0	570	2 A53234	globulin-1S, GIBIS -	4.01e+00
22	55	39.0	504	2 H69333	medium-chain acyl-CoA	4.01e+00
23	55	39.0	775	2 A32494	transposable element	4.01e+00

24	55	39.0	1349	2 T13031	nucleoporin - fruit f	4.01e+00
25	55	39.0	1365	2 T13991	nucleoporin 154 - fru	4.01e+00
26	54	38.3	148	2 E47119	spore coat protein (1	6.34e+00
27	54	38.3	224	1 G64383	riboflavin-specific d	6.34e+00
28	54	38.3	249	2 T04307	M79 protein - rice	6.34e+00
29	54	38.3	249	2 T04335	MADS box protein - ri	6.34e+00
30	54	38.3	259	2 T04169	MADS box protein - ri	6.34e+00
31	54	38.3	562	2 S46281	glycine-rich RNA-bind	9.96e+00
32	54	38.3	818	1 A30107	element - fruit fly	6.34e+00
33	54	38.3	889	2 T11742	dipeptidyl aminopepti	6.34e+00
34	54	38.3	1030	2 S57380	egg sperm receptor -	6.34e+00
35	53	37.6	116	1 Q4ADE2	probable membrane pro	9.96e+00
36	53	37.6	116	1 Q4ADE5	early E4 11k protein	9.96e+00
37	53	37.6	148	2 S41772	glycine-rich RNA-bind	9.96e+00
38	53	37.6	231	2 T14801	MADS box protein MADS	9.96e+00
39	53	37.6	589	2 C38128	epithelin/granulin pr	9.96e+00
40	53	37.6	591	2 S43428	omega-crystallin - g1	9.96e+00
41	53	37.6	669	2 I54205	galactosylceramidase	9.96e+00
42	53	37.6	918	2 D71407	hypothetical protein	9.96e+00
43	53	37.6	1089	1 PFHUGA	platelet-derived grow	9.96e+00
44	53	37.6	1144	2 A54810	TMV resistance protel	9.96e+00
45	53	37.6	2471	2 A49128	cell-fate determining	9.96e+00

ALIGNMENTS

RESULT	ENTRY	1	ALIGNMENTS
TITLE	C5HU	#type complete	
CONTAINS	complement C5 precursor - human		
ORGANISM	Csa anaphylatoxin; C5b		
DATE	#formal_name Homo sapiens #common_name man		
ACCESSIONS	30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999		
REFERENCE	A40075; A27689; A01267; A01266; S15121		
#authors	A40075		
#journal	Haviland, D.L.; Haviland, J.C.; Fleischner, D.T.; Hunt, A.;		
#title	Wetzel, R.A.		
#cross-references	J. Immunol. (1991) 146:362-368		
#accession	Complete cDNA sequence of human complement pro-C5. Evidence		
#molecule_type	of truncated transcripts derived from a single copy gene.		
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567-814,635-670,
702-728,703-735,
715-736,870-1531,
1105-1163,
1379-1509,
1409-1478,
1524-1529,
1536-1609,
1557-1679,
1657-1660
915,1119,1633
#disulfide_bonds #status predicted\
#binding_site carbohydrate (asn) (covalent) #status
predicted
SUMMARY #length 1680 #molecular-weight 188876 #checksum 3888
Query Match 48.9%; Score 69; DB 1; Length 1680;
Best Local Similarity 47.1%; Pred. No. 3.83e-03;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
Db 880 HTSRPSCVFORREGSS 896
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: : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5 QGTGSKRCVROKVEGSS 21

RESULT 3
ENTRY H71862 #type complete
TITLE probable cytochrome C-type biogenesis protein * Helicobacter
ORGANISM pylori (strain J99)
#formal_name Helicobacter pylori
#strain J99
DATE 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
12-Feb-1999
ACCESSIONS H71862
REFERENCE A71800
#authors Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.;
Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge,
B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.;
Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.;
Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Voyls,
G.F.; Trust, T.J
#journal Nature (1999) 397:176-180
#title Genomic sequence comparison of two unrelated isolates of the
human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
#accession H71862
#status preliminary
##molecule_type DNA
##residues 1-936 ##label ARN
##cross-references GB:AE001528; GB:AE001439; NID:g4155575; PID:g4155589
#experimental_source strain J99
GENETICS
#gene jhp1003
SUMMARY #length 936 #molecular-weight 106452 #checksum 7770
Query Match 48.2%; Score 68; DB 2; Length 936;
Best Local Similarity 50.0%; Pred. No. 6.49e-03;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Db 366 IDMHGKSAIEROKIENPA 385
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QY 2 IDHOGTKSKCVROKVEGSS 21

RESULT 4
ENTRY B64567 #type complete
TITLE cytochrome c biogenesis protein - Helicobacter pylori (strain
26695)
ORGANISM #formal_name Helicobacter pylori
DATE 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
10-Oct-1997
ACCESSIONS B64567
REFERENCE A64520
#authors Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutcliffe, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalaf, H.G.; Gilek, A.;
McKenney, K.; Fitzgerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fuji, C.; Bowman, C.; Wathey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
#journal The complete genome sequence of the gastric pathogen
Helicobacter pylori.
#title
#cross-references MUID:97394467
#accession B64567
#status preliminary; nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-936 ##label TOM
#cross-references GB:AE000554; GB:AE000511; NID:g2313475; PID:g2313481;
TIGR:HP0378
SUMMARY #length 936 #molecular-weight 106359 #checksum 8931
Query Match 46.1%; Score 65; DB 2; Length 936;
Best Local Similarity 55.0%; Pred. No. 3.07e-02;
Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Db 366 IDMHGKSAIEROSVENSA 385
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: : : : : : : : : : : : : : : : : : : : : : : : : :
QY 2 IDHOGTKSKCVROKVEGSS 21

RESULT 5
ENTRY T10422 #type complete
TITLE MADS box protein A - white mustard
ORGANISM #formal_name Sinapis alba #common_name white mustard
DATE 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
16-Jul-1999
ACCESSIONS T10422
REFERENCE Z17012
#authors Menzel, G.; Apel, K.; Melzer, S.
#journal Plant J. (1996) 9:399-408
#title Identification of two MADS box genes that are expressed in
the apical meristem of the long-day plant Sinapis alba in
transition to flowering.
#cross-references MUID:97077349
#accession T10422
#status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-213 ##label MEN
#cross-references EMBL:025656; NID:g1199574; PID:g1049022
#experimental_source tissue_type inflorescence meristems
CLASSIFICATION #superfamily transcription factor squa; serum response factor
DNA-binding domain homology
KEYWORDS DNA binding; transcription regulation
SUMMARY #length 213 #molecular-weight 24408 #checksum 2106
Query Match 44.7%; Score 63; DB 2; Length 213;
Best Local Similarity 53.3%; Pred. No. 8.46e-02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Db 127 IEQOLEKSVKCYRAR 141
: : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : :
QY 2 IDHOGTKSKCVROK 16

RESULT 6
ENTRY S76070 #type complete
TITLE hypothetical protein - Synechocystis sp. (strain PCC 6803)
ORGANISM #formal_name Synechocystis sp.
#strain PCC 6803
DATE 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
21-Aug-1998
ACCESSIONS S76070
```



```

Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Db 592 RSRKCVPRKINSN 605
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Qy 8 KSKKCVROKVEGSS 21

RESULT 10
ENTRY A56678 #type complete
TITLE ymanuclain-alpha - fruit fly (Drosophila melanogaster)
ORGANISM #formal.name Drosophila melanogaster
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
24-Sep-1998
ACCESSIONS A56678, S22146
REFERENCE A56678
#authors Alt-Almed, O.; Bellon, B.; Capri, M.; Joblet, C.;
Thomas-Delage, M.
#journal Mech. Dev. (1992) 37:69-80
#title The ymanuclain-alpha: a new Drosophila DNA binding protein
specific for the oocyte nucleus.
#cross-references M01D:92297435
#accession A56678
##status preliminary
##molecule_type DNA
##residues 1-1002 ##label A1E
#cross-references GB:X63503; NID:98837; PID:g8838
GENETICS
#gene FlyBase:yemagr
#cross-references FlyBase:FBgn0005596
#introns 80/3; 154/3; 428/1 477/2; 557/2
KEYWORDS DNA binding; oocyte
SUMMARY #length 1002 #molecular-weight 109310 #checksum 4278

Query Match 41.8%; Score 59; DB 2; Length 1002;
Best Local Similarity 50.0%; Pred. No. 6.08e-01;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db 47 TTKACIRIKLD 58
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Qy 7 TKSKCVROKVE 18

RESULT 11
ENTRY A65068 #type complete
TITLE hypothetical protein b2848 - Escherichia coli (strain K-12)
ORGANISM #formal.name Escherichia coli
DATE 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
14-Nov-1997
ACCESSIONS A65068
REFERENCE A65068
#authors Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kiripatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao
Y.
#journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references M01D:9742617
#accession A65068
##status preliminary; nucleic acid sequence not shown;
translational not shown
##molecule_type DNA
##residues 1-164 ##label BLAT
#cross-references GB:AE000368; GB:U00096; NID:g2367165; PID:g2367166;
UMGP:b2848
SUMMARY ##experimental_source strain K-12, substrain MG1655
#length 164 #molecular-weight 19201 #checksum 281

Query Match 41.1%; Score 58; DB 2; Length 164;
Best Local Similarity 40.0%; Pred. No. 9.82e-01;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Db 78 QQGNRESKIRNIE 92

```

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:|:|:|:|:|:|
OY 4 HOGTSSKCVRKVE 18

RESULT 12
ENTRY 149364 #type complete
TITLE protein tyrosine phosphatase - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
17-Mar-1999

ACCESSIONS
149364
REFERENCE
#authors Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
#journal J. Biol. Chem. (1995) 270:26782-26785
#title A single mutation converts a novel-phosphotyrosine binding
domain into a dual-specificity phosphatase.
#cross-references MUID:96070766
#accession 149364
#status preliminary; translated from GB/EMBL/DBJ

##molecule_type mRNA
##residues 1-205 #label RES
##cross-references EMBL:U34973; NID:q1063624; PID:q1063625
CLASSIFICATION
#superfamily VHL-type dual specificity phosphoprotein
phosphatase homology

FEATURE
36-174
#domain VHL-type dual specificity phosphoprotein
phosphatase homology #label VHL
#length 205 #molecular_weight 23683 #checksum 2745

SUMMARY
Query Match 41.1% Score 58; DB 2; Length 205;
Best Local Similarity 25.0%; Pred. No. 9.82e-01;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 51 ILKKGITHTICIRONEAN 70
OY 1 VIDHGTSSKCVRKVEGS 20
:::| |::|:|:|:|:|:|

RESULT 13
ENTRY 149365 #type complete
TITLE protein tyrosine phosphatase - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
17-Mar-1999

ACCESSIONS
149365
REFERENCE
#authors Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
#journal J. Biol. Chem. (1995) 270:26782-26785
#title A single mutation converts a novel-phosphotyrosine binding
domain into a dual-specificity phosphatase.
#cross-references MUID:96070766
#accession 149365
#status preliminary; translated from GB/EMBL/DBJ

##molecule_type mRNA
##residues 1-223 #label RES
##cross-references EMBL:U34973; NID:q1063624; PID:q1063626
GENERIC
#introns 168/3
CLASSIFICATION
#superfamily VHL-type dual specificity phosphoprotein
phosphatase homology

FEATURE
36-174
#domain VHL-type dual specificity phosphoprotein
phosphatase homology #label VHL
#length 223 #molecular_weight 25416 #checksum 359

SUMMARY
Query Match 41.1% Score 58; DB 2; Length 223;
Best Local Similarity 25.0%; Pred. No. 9.82e-01;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 51 ILKKGITHTICIRONEAN 70
OY 1 VIDHGTSSKCVRKVEGS 20
:::| |::|:|:|:|:|:|

```

```
RESULT 14
ENTRY
TITLE      F70677      #type complete
            hypothetical protein RV3549c - Mycobacterium tuberculosis
            (strain H37Rv)
ORGANISM    #formal_name Mycobacterium tuberculosis
DATE        17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
            26-Aug-1999
ACCESSIONS  F70677
REFERENCE   AF0500
#authors    Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
            C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry
            III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.;
            Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
            Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
            Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
            Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
            Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
            Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.;
            Taylor, K.; Whitehead, S.; Barrell, B.G.
#journal    Nature (1998) 393:537-544
#title      Deciphering the biology of Mycobacterium tuberculosis from
            the complete genome sequence.
#cross-references MUID:98295987
#accession  F70677
#status     preliminary; nucleic acid sequence not shown;
            translation not shown
#molecule_type DNA
#residues   1-259 #label COL
#cross-references GB:282098; GB:AL123456; NID:g3261664; PID:e280727;
            PID:gl66611
#experimental_source strain H37Rv
GENETICS
#gene       RV3549c
CLASSIFICATION #superfamily ribitol dehydrogenase; short-chain alcohol
            dehydrogenase homology
FEATURE
17-185      #domain short-chain alcohol dehydrogenase homology
            #label SADH
SUMMARY      #length 259 #molecular-weight 26855 #checksum 5885
            41.1%; Score 58; DB 2; Length 259;
Query Match Best Local Similarity 36.8%; Pred. No. 9.82e-01;
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
Db 35 VFAEQGATVITCARRVDG 53
|: ||: | | : | : |
QY 1 VIDHQGTSSKCKVRQKVEG 19

RESULT 15
ENTRY
TITLE      I68524      #type complete
            ribosomal protein L34 - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change
            13-Aug-1999
ACCESSIONS  I68524
REFERENCE   I54209
#authors    Rommens, J.M.; Durocher, F.; McArthur, J.; Tonin, P.;
            Leblanc, J.
#journal    Genomics (1995) 28:530-542
#title      Generation of a transcription map at the HSD17B locus
            centromeric to BRCA1 at 17q21.
#cross-references MUID:96039267
#accession  I68524
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues   1-117 #label RES
#cross-references GB:L38941; NID:gl008855; PID:AA041916.1;
            PID:gl008856
CLASSIFICATION #superfamily rat ribosomal protein L34
SUMMARY      #length 117 #molecular-weight 13305 #checksum 4392
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```
Query Match 40.4%; Score 57; DB 2; Length 117;
Best Local Similarity 41.7%; Pred. No. 1.58e+00;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Db 80 GSMCAKCVDRRI 91
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QY 6 GTKSSKCKVRQKV 17
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Search completed: Wed Sep 6 08:17:01 2000
Job time : 19 secs.

RT cleavage at the C-terminus.";
 RL Biochem. J. 273:635-640(1991).
 RN [6]
 RN STRUCTURE BY NMR OF C5A.
 RX MEDLINE; 88309754.
 RA Zuideverweg E.R., Mollison K.W., Henkin J., Carter G.W.;
 RT "Sequence-specific assignments in the 1H NMR spectrum of the human
 RT inflammatory protein C5a";
 RL Biochemistry 27:3568-3580(1988).
 RN [7]
 RN STRUCTURE BY NMR OF C5A.
 RX MEDLINE; 89207527.
 RA Zuideverweg E.R., Nettesheim D.G., Mollison K.W., Carter G.W.;
 RT "Tertiary structure of human complement component C5a in solution
 RT from nuclear magnetic resonance data.";
 RL Biochemistry 28:172-185(1989).
 RN [8]
 RN STRUCTURE BY NMR OF C5A.
 RX MEDLINE; 89274164.
 RA Zuideverweg E.R., Fesik S.W.;
 RT "Heteronuclear three-dimensional NMR spectroscopy of the inflammatory
 RT protein C5a";
 RL Biochemistry 28:2387-2391(1989).
 RN [9]
 RN STRUCTURE BY NMR OF C5A.
 RX MEDLINE; 97160477.
 RA Zhang X., Boyar W., Galakatos N., Gonnella N.C.;
 RT "Solution structure of a unique C5a semi-synthetic antagonist:
 RT implications in receptor binding.";
 RL Protein Sci. 6:65-72(1997).
 RN [10]
 RN STRUCTURE BY NMR OF C5A.
 RX MEDLINE; 9732508.
 RA Zhang X., Boyar W., Toth M.J., Wennogle L., Gonnella N.C.;
 RT "Structural definition of the C5a C terminus by two-dimensional
 RT nuclear magnetic resonance spectroscopy.";
 RL Proteins 28:261-267(1997).
 CC -1- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
 CC SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,
 CC INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
 CC FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYtic
 CC COMPLEX IS ASSEMBLED.
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
 CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
 CC POLYMPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
 CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
 CC -1- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC
 CC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
 CC BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN.
 CC RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA
 CC CHAIN).
 CC -1- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 855
 CC ONWARD DUE TO THE PRESENCE OF AN ALU REPEAT.
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 CC -----
 DR ENBL; M57729; AAA51925.1; -;
 DR ENBL; M65134; AAA51856.1; -;
 DR PIR; A40075; C5HU.
 DR PIR; S15121; S15121.
 DR PDB; 1KJS; 15-MAY-97.
 DR PDB; 1CFA; 17-SEP-97.

DR MIM; 120900; -;
 DR PFAM; PF00207; A2M; 1.
 DR PFAM; PF01835; A2M.N; 1.
 DR PFAM; PF01821; ANATO; 1.
 DR PFAM; PF01759; NTR; 1.
 DR PRINTS; PRO0004; ANAPHYLATOXN.
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; FALSE_NEG.
 DR PROSITE; PS01177; ANAPHYLATOXIN.1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN.2; 1.
 KW Complement pathway; Complement alternate pathway; Glycoprotein;
 KW Plasma; Membrane attack complex; Cytolysis; Inflammatory response;
 KW Signal; Polymorphism; 3D-structure.
 FT SIGNAL 1 18
 FT CHAIN 19 673
 FT PROPEP 674 677
 FT CHAIN 678 1676
 FT PEPTIDE 678 751
 FT CHAIN 752 1676
 FT DOMAIN 698 732
 FT DISULFID 698 724
 FT DISULFID 699 731
 FT DISULFID 711 722
 FT CARBOHYD 741 741
 FT CARBOHYD 911 911
 FT CARBOHYD 1115 1115
 FT CARBOHYD 1630 1630
 FT VARIANT 518 518
 FT SEQUENCE 1676 AA; 188331 MW; 87DCAA63FF977D19 CRC64;
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 Query Match 100.0%; Score 141; DB 1; Length 1676;
 Best Local Similarity 100.0%; Pred. No. 3.33e-25;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 872 VIDHQGTGSKCVQRKVEGSS 892
 QY 1 VIDHQGTGSKCVQRKVEGSS 21
 RESULT 2
 ID COS_MOUSE STANDARD; PRT; 1680 AA.
 AC P06684;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE COMPLEMENT C5 PRECURSOR [CONTAINS: C5A ANAPHYLATOXIN].
 GN C5 OR HC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wetzel R.A., Fleischer D.T., Haviland D.L.;
 RX MEDLINE; 90153853.
 RT "Deficiency of the murine fifth complement component (C5). A 2-base
 RT pair gene deletion in a 5'-exon";
 RL J. Biol. Chem. 265:2435-2440(1990).
 RN [2]
 RP SEQUENCE OF 41-1680 FROM N.A.
 RX MEDLINE; 87185363.
 RA Wetzel R.A., Ogata R.T., Tack B.F.;
 RT "Primary structure of the fifth component of murine complement.";
 RL Biochemistry 26:737-743(1987).
 CC -1- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
 CC SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,
 CC INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
 CC FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYtic
 CC COMPLEX IS ASSEMBLED.
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
 CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF

```

CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae;
CC Rhabditidae; Pelodetinae; Caenorhabditis.
CC [1]
CC SEQUENCE FROM N.A.
CC RA STRAIN-BRISTOL N2;
CC RA Langston Z., Wohlmann P., Gilling B.;
CC RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC CC -1- FUNCTION: INVOLVED IN PROTEIN IMPORT INTO THE MITOCHONDRION.
CC PROBABLY INVOLVED IN TRANSLLOCATION ACROSS THE INNER MEMBRANE. AS A
CC BINDING PROTEIN REQUIRED FOR DRIVING THE IMPORT OF PREPROTEINS.
CC CC RECRUITS MITOCHONDRIAL HSP70 TO DRIVE PROTEIN TRANSLLOCATION INTO
CC THE MATRIX USING ATP AS AN ENERGY SOURCE (BY SIMILARITY).
CC -1- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT
CC LEAST 3 DIFFERENT PROTEINS (TIM17, TIM33, TIM44) (BY SIMILARITY).
CC CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE TIM44 FAMILY.
CC -----
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CC -----
CC DR EMBL; U97405; AAB53011.1; -.
CC DR WORMPEP; T09B4.9; CE13473.
CC KW Mitochondrion; Inner membrane; Transport; Protein transport;
CC KM Translocation; Transit peptide.
CC FT TRANSIT 1 ?
CC FT CHAIN ? 425 MITOCHONDRION.
CC FT MEMBRANE TRANSLLOCATION SUBUNIT TIM44.
CC SQ SEQUENCE 425 AA; 49398 MW; 203DBDBD614E099F8 CRC64;
CC -----
CC Query Match 42.6%; Score 60; DB 1; Length 425;
CC Best Local Similarity 38.9%; Pred. No. 1,11e-01;
CC Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
CC -----
CC Db 85 IVERETLKSSSEVKOKIE 102
CC Qy 1 VIDHGTSSKCVQKVE 18
CC :: : ||| :||:|
CC -----
CC RESULT 4
CC ID IROA_NEIME STANDARD; PRT; 943 AA.
CC AC 006379;
CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 01-FEB-1996 (Rel. 33, Last annotation update)
CC DE IRON-REGULATED OUTER MEMBRANE PROTEIN A PRECURSOR.
CC GN IROA.
CC OS Neisseria meningitidis.
CC SC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN-BNVC;
CC RX MEDLINE; 94011384.
CC RA Petersson A., van der Ley P., Poolman J.T., Tommassen J.;
CC RT "Molecular characterization of the 98-kilodalton iron-regulated outer
CC RL membrane protein of Neisseria meningitidis."
CC CC -1- FUNCTION: UNKNOWN. MAY BE AN IRON-SIDEROPHORE RECEPTOR.
CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.
CC -1- INDUCTION: BY IRON-STARVATION CONDITIONS.
CC -1- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
CC -----
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CC EMBL; X69214; CAA49148.1; -.
DR PFAM; PF00593; TonB_boxC; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
DR PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
KW Outer membrane; Iron transport; Transp; TonB box; Signal; Receptor.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 943 IRON-REGULATED OUTER MEMBRANE PROTEIN A.
FT SIMILAR 826 943 TONB C-TERMINAL BOX.
SQ SEQUENCE 943 AA; 105424 MW; 5AC578F5C84D8641 CRC64;
Query Match 41.8%; Score 59; DB 1; Length 943;
Best Local Similarity 50.0%; Pred. No. 1.88e-01;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Db 595 RSRKCVPRKINGN 608
:| ||| :|||:
QY 8 KSKKCVQRKVEGSS 21
-----
RESULT 5
ID YEMA_DROME STANDARD; PRT; 1002 AA.
AC P25992;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE YEMANUCLEIN-ALPHA.
GN YEMA OR YG4.5.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE; 92297435.
RA Ait-Ahmed O., Bellon B., Capri M., Joblet C., Thomas-Delaage M.;
RT "The yemanuclein-alpha: a new Drosophila DNA binding protein specific
for the oocyte nucleus."
RL Mech. Dev. 37:69-80(1992).
CC -!- FUNCTION: MAY PLAY A KEY ROLE IN EGG ORGANIZATION. IT MAY BE A
TRANSCRIPTIONAL REGULATOR.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- TISSUE SPECIFICITY: OOCYTE-SPECIFIC.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT ALL OOGENIC STAGES.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
-----
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-----
CC EMBL; X63503; CAA45074.1; -.
DR PIR; S22146; S22146.
DR FLYBASE; FBgn0005596; yem-alpha.
KW Nuclear protein; DNA-binding; Repeat.
FT DOMAIN 80 85 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 207 217 POLY-SER.
FT DOMAIN 219 261 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 230 253 2 X 12 AA TANDEM REPEATS.
FT REPEAT 230 241 1.
FT REPEAT 242 253 2.
FT VARIANT 698 698 S -> L (IN CDNA SEQUENCE).
FT SEQUENCE 1002 AA; 109310 MW; EE69A384EBA24D2F CRC64;
Query Match 41.8%; Score 59; DB 1; Length 1002;
Best Local Similarity 50.0%; Pred. No. 1.88e-01;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db 47 TKTAKCIRIKLD 58
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QY 7 TKSSKCVQRKVE 18
:| |||:| | :| :|
-----
RESULT 6
ID YQBJ_ECOLI STANDARD; PRT; 160 AA.
AC Q46943; P77135;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 18.7 KDA PROTEIN IN KDU1-LYSS INTERGENIC REGION.
GN YQBJ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE OF 34-160 FROM N.A.
RC STRAIN=K12 / MG1655;
RA Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -----
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-----
CC EMBL; U29581; AAB40495.1; ALT_INIT.
DR EMBL; AE000368; AAC75887.1; ALT_INIT.
DR EMBL; U83187; AAB40287.1; -.
DR ECOGENE; EG13101; Yqej.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 8 28 POTENTIAL.
SQ SEQUENCE 160 AA; 18719 MW; 10910D39F2B5F70D CRC64;
Query Match 41.1%; Score 58; DB 1; Length 160;
Best Local Similarity 40.0%; Pred. No. 3.19e-01;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Db 74 QQGNRESKIRNIE 88
:| ||:| | :| :|
QY 4 HQGTKSKCVQRKVE 18
-----
RESULT 7
ID RL34_HUMAN STANDARD; PRT; 116 AA.
AC P49207;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE 60S RIBOSOMAL PROTEIN L34.
GN RPL34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY;
RX MEDLINE; 96039267.
-----
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RA Rommens J.M., Durocher F., McArthur J., Tonin P., Leblanc J.F.,
RA Allen T., Samson C., Feril L., Nard S., Morgan K., Simard J.,
RT "Generation of a transcription map at the HSD17B locus centromeric to
RT BRCA1 at 17q21.";
RL Genomics 28:530-542(1995).
RN [12]
RP SEQUENCE OF 3-47 FROM N.A.
RX MEDLINE; 98248690.
RA Kennoch J.N., Kawaguchi T., Rozen S., Davis E., Goodman N.,
RT Hudson T.J., Tanaka T., Page D.C.;
RT "A map of 75 human ribosomal protein genes.";
RL Genome Res. 8:509-523(1998).
CC -1- SIMILARITY: BELONGS TO THE L34E FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC
CC EMBL; L38941; AAC41916.1; -
DR EMBL; AB007181; BA25840.1; -
DR PFAM; PF01199; Ribosomal_L34e; 1.
DR PROSITE; PS01145; RIBOSOMAL_L34E; 1.
KW Ribosomal protein.
FT INIT MET 0
SQ SEQUENCE 116 AA; 13174 MW; 0C1EBA2AACA5D3 CRC64;
BY SIMILARITY.
Query Match 40.4%; Score 57; DB 1; Length 116;
Best Local Similarity 41.7%; Pred. No. 5,36e-01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Db 79 GSKACVCVRRI 90
1:::|||||:::
6 GTRSSKCVQKRV 17
RESULT 8
ID CSH_ARTSP STANDARD; PRT; 264 AA.
AC P32400;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE N-CARBAMOYLARSOSINE AMIDASE (EC 3.5.1.59) (N-CARBAMOYLARSOSINE
DE AMIDOHYDROLASE) (CSHASE).
OS Arthrobacter sp.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Micrococcales; Micrococcaceae; Arthrobacter.
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISIONS TO 184 AND 232.
RX MEDLINE; 92389321.
RA Romao M.J., Turk D., Gomis-Rueth F.-X., Huber R.;
RT "Crystal structure analysis, refinement and enzymatic reaction
RT mechanism of N-carbamoylarsosine amidohydrolase from Arthrobacter
RT sp. at 2.0-A resolution.";
RL J. Mol. Biol. 226:1111-1130(1992).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.28 ANGSTROMS) OF COMPLEX WITH INHIBITORS.
RX MEDLINE; 97070380.
RA Zajc A., Romao M.J., Turk D., Huber R.;
RT "Crystallographic and fluorescence studies of ligand binding to N-
RT carbamoylarsosine amidohydrolase from Arthrobacter sp.";
RL J. Mol. Biol. 263:269-283(1996).
CC -1- CATALYTIC ACTIVITY: N-CARBAMOYLARSOSINE + H(2)O = SAROSINE +
CC CO(2) + NH(3).
CC -1- COFACTOR: ONE SULFATE ION PER SUBUNIT.
CC -1- PATHWAY: DEGRADATION OF CREATININE TO GLYCINE.
CC -1- SUBUNIT: HOMOTETRAMER.
DR PIR; S28969; S28969.
DR PDB; 1NBA; 22-JUN-94.
DR PFAM; PF00857; Isochorismatase; 1.
RN

KW Hydrolase; 3D-structure.
FT ACT_SITE 177 177 INVOLVED IN HYDROLYSIS OF THE SUBSTRATE.
SQ SEQUENCE 264 AA; 29057 MW; 8A213B555EA5DCDC CRC64;
Query Match 40.4%; Score 57; DB 1; Length 264;
Best Local Similarity 40.0%; Pred. No. 5,36e-01;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Db 171 GATAGCVRRTVEDA 185
1:::|||||:::
6 GTRSSKCVQKVEGS 20
Query Match 39.7%; Score 56; DB 1; Length 89;
Best Local Similarity 60.0%; Pred. No. 8,95e-01;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Db 64 GAKGKCVQK 73
1:::|||||:::
6 GTRSSKCVQK 15
RESULT 10
ID SP70_DICDI STANDARD; PRT; 537 AA.
AC P15269; P08126;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SPORE COAT PROTEIN SP70 PRECURSOR (BREVIN PROTEIN).
GN COTB.
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Dictyostelida; Dictyostelium.
RN [1]
RESULT 9
ID IT16_ARATH STANDARD; PRT; 89 AA.
AC O22869;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PURATIVE TRYPSIN INHIBITOR T01024.29 PRECURSOR.
GN T01024.29.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
OC Brassicaceae; Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Roundley S.D., Tschudy M.M., Lin X., Ketchum K.A., Crosby M.L.,
RA Brandon R.C., Spriggs T.A., Mason T.M., Kervilave A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (Jul-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE RT1/MR1-2 PROTEASE INHIBITORS FAMILY.
CC -----
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CC -----
CC
CC EMBL; AC002335; AAB64322.1; -
DR Serine protease inhibitor; Signal; Multigene family.
KW SIGNAL 1 26
FT CHAIN 27 89 POTENTIAL.
FT DISULFID 33 86 POTATIVE TRYPSIN INHIBITOR T01024.29.
FT DISULFID 46 70 BY SIMILARITY.
FT DISULFID 55 81 BY SIMILARITY.
FT DISULFID 59 83 BY SIMILARITY.
FT ACT_SITE 49 50 REACTIVE-BOND (BY SIMILARITY).
SQ SEQUENCE 89 AA; 10192 MW; C0964810F33099A3 CRC64;
Query Match 39.7%; Score 56; DB 1; Length 89;
Best Local Similarity 60.0%; Pred. No. 8,95e-01;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Db 64 GAKGKCVQK 73
1:::|||||:::
6 GTRSSKCVQK 15
RESULT 10
ID SP70_DICDI STANDARD; PRT; 537 AA.
AC P15269; P08126;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SPORE COAT PROTEIN SP70 PRECURSOR (BREVIN PROTEIN).
GN COTB.
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Dictyostelida; Dictyostelium.
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE; 90097939.
RA Fosnaugh K.L., Loomis W.F.;
RT "Spore coat genes SP60 and SP70 of Dictyostelium discoideum.";
RN J. Cell Biol. 9:5215-5218(1989).
RP PRELIMINARY SEQUENCE OF 72-170 FROM N.A.
RX MEDLINE; 87057653.
RA Gomer R.H., Datta S., Firtel R.A.;
RT "Cellular and subcellular distribution of a cAMP-regulated prestalk
protein and prespore protein in Dictyostelium discoideum: a study on
the ontogeny of prestalk and prespore cells.";
RL J. Cell Biol. 103:1999-2015(1986).
CC -!- PTM: PHOSPHORYLATED AND FUCOSYLATED.
CC -!- SIMILARITY: CONTAINS 3 PRESPORE MOTIFS.
CC -----
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CC -----
CC EMBL; M26238; AAA33252.1; -.
DR DR M26238; AAA33252.1; -.
DR PIR; B33485; B33485.
DR PIR; B25439; B25439.
DR DICTYDB; DD03009; COTB.
KW Glycoprotein; Phosphorylation; Repeat; Sporulation; Signal.
FT SIGNAL 1 20
FT CHAIN 21 537 SPORE COAT PROTEIN SP70.
FT DOMAIN 182 250 SER/THR-RICH.
FT DOMAIN 190 248 5.5 X 11 AA TANDEM REPEATS.
FT REPEAT 190 200 1.
FT REPEAT 191 211 2.
FT REPEAT 212 222 3.
FT REPEAT 223 233 4.
FT REPEAT 234 244 5.
FT REPEAT 245 248 6 (INCOMPLETE).
FT REPEAT 251 263 PRESPORE MOTIF 1.
FT REPEAT 279 291 PRESPORE MOTIF 2.
FT REPEAT 359 371 PRESPORE MOTIF 3.
FT CARBOHYD 97 POTENTIAL.
SQ SEQUENCE 537 AA; 56650 MW; 0EA20BDC96DE2A19 CRC64;

Query Match 39.7%; Score 56; DB 1; Length 537;
Best Local Similarity 54.5%; Pred. No. 8.95e-01;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 291 KNGECIRDKVE 301
|::|:|:|:|
QY 8 KSSKCVQKVE 18

RESULT 11
ID GLB1-MAIZE STANDARD; PRT; 573 AA.
AC P15590;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GLOBULIN-1 S ALLELE PRECURSOR (GLB1-S) (7S-LIKE).
GN GLB1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. INBRED LINE VA26;
RA Belanger F.C., Kriz A.L.;
RT "Molecular characterization of the major maize embryo globulin encoded
by the Glb1 gene.";
RL Plant Physiol. 91:636-643(1989).
RN [2]

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RP SEQUENCE OF 87-100.
RX MEDLINE; 89374022.
RA Kriz A.L.;
RT "Characterization of embryo globulins encoded by the maize Glb
genes.";
RL Biochem. Genet. 27:239-251(1989).
CC -!- PTM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF THE
MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
CC -!- POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GLB1 ALLELES HAVE
THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL
PROTEINS, RESPECTIVELY.
CC -!- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CONVICILIN, CONGLYCININ, ETC.).
CC -----
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CC -----
CC EMBL; M24845; AAA33467.1; -.
DR DR M24845; AAA33467.1; -.
DR HSSP; P50477; ICAW.
DR MAIZEDB; 30181; -.
DR PFAM; PF00546; Seedstore_7s; 1.
KW Seed storage protein; Signal. OR 21 (POTENTIAL).
FT SIGNAL 1 18
FT PROPEP 19 86
FT CHAIN 87 573 GLOBULIN-1 S ALLELE.
FT CARBOHYD 349 349 POTENTIAL.
SQ SEQUENCE 573 AA; 65029 MW; 525EDID00A062976 CRC64;

Query Match 39.7%; Score 56; DB 1; Length 573;
Best Local Similarity 58.3%; Pred. No. 8.95e-01;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 32 HGGHSGRCVRR 43
|::|:|:|:|
QY 4 HGGTSSKCVQ 15

RESULT 12
ID RPOB_PSEPU STANDARD; PRT; 1357 AA.
AC P19175;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE BETA CHAIN (PC 2.7.7.6) (TRANSCRIPTASE
BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT).
GN RPOB.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RA Borodin A.M., Danilkovich A.V., Allikmets R.L., Rostapshov V.M.,
RA Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.;
RT "Nucleotide sequence of the rpoB gene coding for the beta-subunit of
RNA polymerase in Pseudomonas putida.";
RL Dokl. Biochem. 302:1261-1265(1988).
RN [2]
RP SEQUENCE OF 1036-1357 FROM N.A.
RX MEDLINE; 89117617.
RA Borodin A.M., Danilkovich A.V., Chernov I.P., Azhikina T.L.,
RA Rostapshov V.M., Monastyrskaya G.S.;
RT "Genes coding for RNA polymerase in bacteria. III. The use of
modified Sanger's method for sequencing the C-terminal region of rpoB
gene, N-terminal region of rpoC gene and intercistron region of RNA
polymerase in Pseudomonas putida.";
RL Bioorg. Khim. 14:1179-1182(1988).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

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CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE -> N PYROPHOSPHATE +
CC RNA(N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
CC -----
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CC -----
CC EMBL: X15849; CAA33846.1; -
CC DR EMBL: M88319; AAA25986.1; -
CC DR PIR: P00362; RNA_POL_B; 1.
CC DR PROSITE: PS01166; RNA_POL_BETA; 1.
CC FT TRANSFERASE; Transcription; DNA-directed RNA polymerase.
CC FT CONFLICT 1180 1180 T -> N (IN REF. 2).
CC FT CONFLICT 1184 1184 I -> V (IN REF. 2).
CC FT CONFLICT 1236 1236 F -> S (IN REF. 2).
CC SQ SEQUENCE 1357 AA; 151305 MW; 4AEDB68C8B086EA6 CRC64;

Query Match 39.7%; Score 56; DB 1; Length 1357;
Best Local Similarity 41.2%; Pred. No. 8,956-01;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 450 IDHGNRRVRCVGEAE 466
||| | :|| :|
QY 2 IDHGNRRVRCVGEAE 18

RESULT 13
ID YTX1_XENLA STANDARD; PRT; 775 AA.
AC P14380;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE TRANSDUCED T1 HYPOPHOSPHATE 82 KDA PROTEIN (OFR 1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89384562.
RA Garrett J.E., Knutson D.S., Carroll D.;
RT *Composite transposable elements in the Xenopus laevis genome.*;
RL Mol. Cell. Biol. 9:3018-3027(1989).
CC -----
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CC -----
CC EMBL: M26915; AAA49975.1; -
CC DR EMBL: A32494; A32494.
CC DR PRINTS: PR00939; C2HCZNFINGER.
CC KW Hypothetical protein; Transposable element.
CC SQ SEQUENCE 775 AA; 82355 MW; B8C361AEC65DD85B CRC64;

Query Match 39.0%; Score 55; DB 1; Length 775;
Best Local Similarity 46.7%; Pred. No. 1,486+00;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 617 SNTSKVSSEVEGTP 631
:::||||| |||::

QY 7 TKSKCKVRQKVEGSS 21

RESULT 14
ID COT2_BACSU STANDARD; PRT; 148 AA.
AC Q08312;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE SPORE COAT PROTEIN 2.
GN COT2.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168 / JH642;
RX MEDLINE: 93285989.
RA Zhang J., Fitz-James P.C., Aronson A.I.;
RT "Cloning and characterization of a cluster of genes encoding
RT polypeptides present in the insoluble fraction of the spore coat of
RT Bacillus subtilis".
RL J. Bacteriol. 173:3757-3766(1993).
CC -1- SUBUNIT: DISULFIDE CROSS-LINKED EITHER TO ITSELF OR TO COTY.
CC -1- SUBCELLULAR LOCATION: SPORE OUTER COAT.
CC -1- SIMILARITY: TO COTY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L10116; AAA22329.1; -
CC DR EMBL: 299110; CAB13031.1; -
CC DR PIR: EA7119; E47119.
CC DR SUBTILIST; BG10439; COT2.
CC KW Sporulation.
CC SQ SEQUENCE 148 AA; 16534 MW; 90429FFB050896E CRC64;

Query Match 38.3%; Score 54; DB 1; Length 148;
Best Local Similarity 63.6%; Pred. No. 2,446+00;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 4 KTSCVREAVE 14
|:| ||| :|
QY 8 KSKCKVRQKVE 18

RESULT 15
ID R1B7_METJA STANDARD; PRT; 224 AA.
AC Q58085;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PUTATIVE 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL REDUCTASE
DE (EC 1.1.1.193) (HTP REDUCTASE).
GN Mj0671.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE: 96337999.
RA But C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervase A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback L.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

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RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -!- CATALYTIC ACTIVITY: 5-AMINO-6-(5-PHOSPHORIBITYLAMINO)URACIL +
CC NADP(+) = 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL + NADPH.
CC -!- PATHWAY: THIRD STEP OF RIBOFLAVIN BIOSYNTHESIS.
CC -!- SIMILARITY: BELONGS TO THE HTP REDUCTASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U67514; AAB98665.1; -.
DR TIGR; MJ0671; -.
DR PFAM; PF01872; RibD_C; 1.
KW Hypothetical protein: Riboflavin biosynthesis; Oxidoreductase; NADP.
SQ SEQUENCE 224 AA; 25037 MW; 4D8C15CE291E89D8 CRC64;

Query Match      38.3%; Score 54; DB 1; Length 224;
Best Local Similarity 33.3%; Pred. No. 2.44e+00;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 118 ILEDMGVEVVKCGRGVD 135
QY 1 VIDHOGTKSKCVQRKVE 18
::: | || | |

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Search completed: Wed Sep 6 08:15:32 2000
 Job time : 12 secs.

 RELEASE
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Title: >US-08-487-283A-1
 Description: (1-21) from US08487283A.pep
 Perfect Score: 141
 Sequence: 1 VIDHGTGKSKCVROKVEGSS 21

Scoring table: PAM 150
 Gap 15

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: spiremb12
 1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
 5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
 9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
 13:sp-vertebrate 14:sp-virus

Statistics: Mean 25.849; Variance 31.531; scale 0.820

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	68	48.2	936	2	Q9ZKD6	PUTATIVE CYTOCHROME C-	8.98e-03
2	65	46.1	936	2	Q25141	CYTOCHROME C BIOGENESI	4.33e-02
3	64	45.4	543	2	Q9X7U3	PUTATIVE PROTEASE	7.25e-02
4	63	44.7	213	10	Q41275	TRANSCRIPTION FACTOR S	1.21e-01
5	62	44.0	213	2	Q53530	HYPOHETICAL 22.7 KD P	2.00e-01
6	61	43.3	214	10	Q64645	MADS BOX PROTEIN AG120	3.31e-01
7	60	42.6	1166	5	Q96219	HYPOHETICAL 139.4 KD	5.44e-01
8	59	41.8	940	2	Q51187	LACTOFERRIN BINDING PR	8.88e-01
9	59	41.8	943	2	Q87343	LACTOFERRIN BINDING PR	8.88e-01
10	59	41.8	943	2	Q50952	LACTOFERRIN RECEPTOR	8.88e-01
11	58	41.1	205	11	Q60969	PROTEIN TYROSINE PHOSP	1.44e+00
12	58	41.1	223	11	Q60970	PROTEIN TYROSINE PHOSP	1.44e+00
13	58	41.1	259	2	P71852	HYPOHETICAL 26.8 KD P	1.44e+00
14	58	41.1	451	5	P90814	F46C5.9 PROTEIN.	1.44e+00
15	58	41.1	972	5	Q26614	FIBROBLAST GROWTH FACT	1.44e+00
16	57	40.4	963	4	Q94829	KIAA0724 PROTEIN.	2.33e+00
17	56	39.7	80	14	Q84420	A99L PROTEIN.	3.75e+00
18	56	39.7	236	10	Q81250	GLOBULIN-1 (FRAGMENT)	3.75e+00
19	56	39.7	236	10	Q81254	GLOBULIN-1 (FRAGMENT)	3.75e+00
20	56	39.7	238	10	Q81257	GLOBULIN-1 (FRAGMENT)	3.75e+00

Result ID	Score	Match	Length	DB	ID	Description	Pred. No.
1	68	48.2	936	2	Q9ZKD6	PUTATIVE CYTOCHROME C-	8.98e-03
2	65	46.1	936	2	Q25141	CYTOCHROME C BIOGENESI	4.33e-02
3	64	45.4	543	2	Q9X7U3	PUTATIVE PROTEASE	7.25e-02
4	63	44.7	213	10	Q41275	TRANSCRIPTION FACTOR S	1.21e-01
5	62	44.0	213	2	Q53530	HYPOHETICAL 22.7 KD P	2.00e-01
6	61	43.3	214	10	Q64645	MADS BOX PROTEIN AG120	3.31e-01
7	60	42.6	1166	5	Q96219	HYPOHETICAL 139.4 KD	5.44e-01
8	59	41.8	940	2	Q51187	LACTOFERRIN BINDING PR	8.88e-01
9	59	41.8	943	2	Q87343	LACTOFERRIN BINDING PR	8.88e-01
10	59	41.8	943	2	Q50952	LACTOFERRIN RECEPTOR	8.88e-01
11	58	41.1	205	11	Q60969	PROTEIN TYROSINE PHOSP	1.44e+00
12	58	41.1	223	11	Q60970	PROTEIN TYROSINE PHOSP	1.44e+00
13	58	41.1	259	2	P71852	HYPOHETICAL 26.8 KD P	1.44e+00
14	58	41.1	451	5	P90814	F46C5.9 PROTEIN.	1.44e+00
15	58	41.1	972	5	Q26614	FIBROBLAST GROWTH FACT	1.44e+00
16	57	40.4	963	4	Q94829	KIAA0724 PROTEIN.	2.33e+00
17	56	39.7	80	14	Q84420	A99L PROTEIN.	3.75e+00
18	56	39.7	236	10	Q81250	GLOBULIN-1 (FRAGMENT)	3.75e+00
19	56	39.7	236	10	Q81254	GLOBULIN-1 (FRAGMENT)	3.75e+00
20	56	39.7	238	10	Q81257	GLOBULIN-1 (FRAGMENT)	3.75e+00

ALIGNMENTS

Result ID	Score	Match	Length	DB	ID	Description	Pred. No.
1	68	48.2	936	2	Q9ZKD6	PUTATIVE CYTOCHROME C-	8.98e-03
2	65	46.1	936	2	Q25141	CYTOCHROME C BIOGENESI	4.33e-02
3	64	45.4	543	2	Q9X7U3	PUTATIVE PROTEASE	7.25e-02
4	63	44.7	213	10	Q41275	TRANSCRIPTION FACTOR S	1.21e-01
5	62	44.0	213	2	Q53530	HYPOHETICAL 22.7 KD P	2.00e-01
6	61	43.3	214	10	Q64645	MADS BOX PROTEIN AG120	3.31e-01
7	60	42.6	1166	5	Q96219	HYPOHETICAL 139.4 KD	5.44e-01
8	59	41.8	940	2	Q51187	LACTOFERRIN BINDING PR	8.88e-01
9	59	41.8	943	2	Q87343	LACTOFERRIN BINDING PR	8.88e-01
10	59	41.8	943	2	Q50952	LACTOFERRIN RECEPTOR	8.88e-01
11	58	41.1	205	11	Q60969	PROTEIN TYROSINE PHOSP	1.44e+00
12	58	41.1	223	11	Q60970	PROTEIN TYROSINE PHOSP	1.44e+00
13	58	41.1	259	2	P71852	HYPOHETICAL 26.8 KD P	1.44e+00
14	58	41.1	451	5	P90814	F46C5.9 PROTEIN.	1.44e+00
15	58	41.1	972	5	Q26614	FIBROBLAST GROWTH FACT	1.44e+00
16	57	40.4	963	4	Q94829	KIAA0724 PROTEIN.	2.33e+00
17	56	39.7	80	14	Q84420	A99L PROTEIN.	3.75e+00
18	56	39.7	236	10	Q81250	GLOBULIN-1 (FRAGMENT)	3.75e+00
19	56	39.7	236	10	Q81254	GLOBULIN-1 (FRAGMENT)	3.75e+00
20	56	39.7	238	10	Q81257	GLOBULIN-1 (FRAGMENT)	3.75e+00

```

OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=26695;
RC MEDLINE; 97394467.
RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
RA LOFTUS B., RICHARDSON D., DODSON R., ADAMS H.G., GLODEK A.,
RA MCKENNEY K., FITZGERALD L.M., LEE N., KHALAK M.D., HICKEY E.K.,
RA BERG D.E., GOCAYNE J.D., PETERSON J.D., KELLEY J.M.,
RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.,
RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
RA VENTER J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000554; AAD07446.1; -.
DR TIGR; HF0378; -.
DR PFAM; PF01578; CytC_asm; 2.
KW Hypothetical protein.
SQ SEQUENCE 936 AA; 106359 MW; F1D27C55 CRC32;

Query Match 46.1%; Score 65; DB 2; Length 936;
Best Local Similarity 55.0%; Pred. No. 4.33e-02;
Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 366 IDMHGKSAKIERQSVNSA 385
QY 2 IDHQGTSSKCVKQKVEGS 21

RESULT 3
ID Q9X7U3 PRELIMINARY; PRT; 543 AA.
AC Q9X7U3;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE PUTATIVE PROTEASE.
GN SC5H1.36.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA OLIVER K., HARRIS D.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA JAMES K.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA REDENBACH M., KIESER H.M., DENAPATE D., EICHNER A., CULLUM J.,
RA KINASHI H., HOPWOOD D.A.;
RL "A set of ordered cosmids and a detailed genetic and physical map for
RL the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
DR Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL049863; CAB42961.1; -.
KW Protease.
SQ SEQUENCE 543 AA; 57696 MW; 0F49B825 CRC32;

Query Match 45.4%; Score 64; DB 2; Length 543;
Best Local Similarity 60.0%; Pred. No. 7.25e-02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db 504 HTGYASSKCVHRKVD 518
QY 4 HOGTKSSKCVKQKVE 18

RESULT 4
ID Q41275 PRELIMINARY; PRT; 213 AA.
AC Q41275;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE TRANSCRIPTION FACTOR SAMADS A.
GN MADS.
OS Sinapis alba (White mustard) (Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Sinapis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INFLUENCE MERISTEMS;
RX MEDLINE; 97077349.
RA MENZEL G., APEL K., MELZER S.;
RT "Identification of two MADS box genes that are expressed in the apical
RT meristem of the long-day plant Sinapis alba in transition to
RT flowering.";
RL Plant J. 9:399-408(1996).
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -|- SIMILARITY: CONTAINS A DOMAIN FOUND IN SRF-TYPE TRANSCRIPTION
CC FACTORS (MADS-DOMAIN).
DR EMBL; U25696; AAB41526.1; -.
DR HSSP; P11746; 1MNM.
DR MENDEL; 10511; Sinal; MADS; 10511.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PFAM; PF01486; K-box; 1.
DR PFAM; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
KW Transcription regulation; DNA-binding; Nuclear protein.
SQ SEQUENCE 213 AA; 24408 MW; 0562BB62 CRC32;

Query Match 44.7%; Score 63; DB 10; Length 213;
Best Local Similarity 53.3%; Pred. No. 1.21e-01;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 127 IEQQLKSVKCVRAR 141
QY 2 IDHQGTSSKCVKQKVE 16

RESULT 5
ID Q55550 PRELIMINARY; PRT; 213 AA.
AC Q55550;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)
DE HYPOTHETICAL 22.7 KD PROTEIN.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC6803;
RA TABATA S.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC6803;
RX MEDLINE; 96127529.
RA KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N.,
RA SUGIURA M., TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
DR DNA Res. 2:153-166(1995).

```

RN	[3]	SEQUENCE FROM N.A.
RP		STRAIN-PC6803;
RC		MEDLINE; 97061201.
RA	KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,	
RA	MIRAJALVA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,	
RA	HOSOUCHI T., MATSUONO A., MURAKI A., NAKAZAKI N., NARAO K., OKUMURA S.,	
RA	SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,	
RA	TANATA S.;	
RT	"Sequence analysis of the genome of the unicellular cyanobacterium	
RT	Synechocystis sp. strain PC6803. II. Sequence determination of the	
RT	entire genome and assignment of potential protein-coding regions.";	
RL	DNA Res. 3:109-136(1996).	
DR	EMBL; D63999; BAA10048.1; -.	
KW	Hypothetical protein.	
SO	SEQUENCE 213 AA; 22745 MW; 88506910 CRC32;	
<hr/>		
Db	92 ILAVIGANASDCIRPKVVS 111	
Oy	1 VIDHGTKSKCVRKVEGS 20	
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RESULT	6	
ID	064645	PRELIMINARY; PRT; 214 AA.
AC	064645;	
DT	01-AUG-1998 (TREMblrel. 07, Created)	
DT	01-AUG-1998 (TREMblrel. 07, Last sequence update)	
DT	01-NOV-1999 (TREMblrel. 12, Last annotation update)	
DE	MADS BOX PROTEIN AG120.	
GN	MADS OR F17K2.19.	
OS	Aralidopsis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;	
CC	corte eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;	
CC	Arabidopsis.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-CV. COLUMBIA;	
RA	ROUNISLEY S.D., KAUL S., LIN X., KETCHUM K.A., CROSSBY M.L.,	
RA	BRANDON R.C., STOKES S.M., MASON T.M., KERLAUGE A.R., ADAMS M.D.,	
RA	SOMERVILLE C.R., VENTER J.C.;	
RL	submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.	
CC	-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).	
CC	-I- SIMILARITY: CONTAINS A DOMAIN FOUND IN SRP-TYPE TRANSCRIPTION	
CC	FACTORS (MADS-DOMAIN).	
CC	EMBL; AC003680; AAC06175.1; -.	
DR	HSSP; P11746; 1MMN.	
DR	MENDEL; 29412; Arath;MADS;29412.	
DR	PROSITE; PS00350; MADS_BOX_1; 1.	
DR	Pfam; PF01486; K-box; 1.	
DR	Pfam; PF00319; SRP-TF; 1.	
DR	PRINTS; PR00404; MADSDOMAIN.	
DR	Transcription regulation; DNA-binding; Nuclear protein.	
KW	SEQUENCE 214 AA; 24533 MW; EZD3914C CRC32;	
SO	SEQUENCE	
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Query Match	43.3%;	Score 61; DB 10; Length 214;
Best Local Similarity	46.7%;	Fred. No. 3.31e-01;
Matches	7; Conservative	4; Mismatches 4; Indels 0; Gaps 0;
Db	127 IEOLERSVCICRAR 141	
Oy	2 IDHGTKSKCVRK 16	
<hr/>		
RESULT	7	
ID	096219	PRELIMINARY; PRT; 1166 AA.
AC	096219;	
DT	01-MAY-1999 (TREMblrel. 10, Created)	
DT	01-MAY-1999 (TREMblrel. 10, Last sequence update)	

DT	01-MAY-1999 (TReMBLrel_10, Last annotation update)
DE	HYPOTHETICAL 139.4 KD PROTEIN.
GN	P8B0630C.
OS	Plasmodium falciparum.
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN	[1]
RP	SEQUENCE FROM N.A.
KX	MEDLINE; 99021743.
RA	GARDNER M.J., TETTELIN H., CARUCCI D.J., CUMMINGS L.M., ARAVIND L., KOONIN E.V., SHALLOO S., MASON T., YU K., FUJII C., PEDERSON J., SHEN K., JING J., ASTON C., LAI Z., SCHWARTZ D.C., PERREA M., SALZBERG S., ZHOU L., SUTTON G.G., CLATTON R., WHITE O., SMITH H.O., FRASER C.M., ADAMS M.D., VENTER J.C., HOFFMAN S.L.; "Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum";
RT	Science 282:1126-1132(1998).
RL	EMBL; AE001407; AAC11915.1; ..
KW	Hypothetical protein.
SQ	SEQUENCE 1166 AA; 139389 MW; D72D31F8 CRC32;
Dd	Query Match 42.6%; Score 60; DB 5; Length 1166; Best Local Similarity 43.8%; Pred.No. 5,44e-01; Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
OY	3 DHOGTKSKCVORKE 18 : : : :
RESULT 8	
ID	Q51187 PRELIMINARY; PRT; 940 AA.
AC	Q51187;
DT	01-NOV-1996 (TReMBLrel_01, Created)
DR	01-NOV-1996 (TReMBLrel_01, Last sequence update)
DT	01-NOV-1998 (TReMBLrel_08, Last annotation update)
DE	LACTOFERRIN BINDING PROTEIN.
GN	LBPA.
OS	Neisseria meningitidis.
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN	[1]
RP	SEQUENCE FROM N.A.
KC	STRAIN-H44/76;
KX	MEDLINE; 95272374.
RA	PETERSSON A.M., KLARENBEK V., VAN DEURZEN J., POOLMAN J.T., TOMMASSEN J.;
RT	"Molecular characterization of the structural gene for the lactoferrin receptor of the meningococcal strain H44/76.";
RL	Microb. Pathog. 17:395-408(1994).
DR	EMBL; X79838; CAA56233.1; ..
DR	PFAM; PF00593; TonB_boxC; 1.
SQ	SEQUENCE 940 AA; 105347 MW; 01ACA021 CRC32;
Dd	Query Match 41.8%; Score 59; DB 2; Length 940; Best Local Similarity 50.0%; Pred.No. 8,88e-01; Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
OY	8 KSKCKVRKGVGS 21 : : :
Db	592 RSRKCPRKNGSN 605 : : :
Qy	8 KSKCKVRKGVGS 21
RESULT 9	
ID	087343 PRELIMINARY; PRT; 943 AA.
AC	087343;
DT	01-NOV-1998 (TReMBLrel_08, Created)
DT	01-NOV-1998 (TReMBLrel_08, Last sequence update)
DT	01-MAY-1999 (TReMBLrel_10, Last annotation update)
DE	LACTOFERRIN BINDING PROTEIN A PRECURSOR.
GN	LBPA.
OS	Neisseria meningitidis.
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN	[1]
RP	SEQUENCE FROM N.A.

```

RC STRAIN=DNM2;
RX MEDLINE; 98261564.
RA LEWIS L.A., ROHDE K., GIPSON M., BEHRENS B., GRAY E., TOTH S.I.,
RA ROE B.A., DYER D.W.;
RT Identification and molecular analysis of lbpa, which encodes the
RT two-component meningococcal lactoferrin receptor.";
RL Infect. Immun. 66:3017-3023(1998).
DR EMBL; AF049349; AAC35271.1; -.
DR PFAM; PF00593; TonB_boxC; 1.
KW Signal.
FT SIGNAL
FT CHAIN 1 24
FT CHAIN 24 943 LACTOFERRIN BINDING PROTEIN A.
SQ SEQUENCE 943 AA; 105426 MW; 087E2FC6 CRC32;

Query Match 41.8%; Score 59; DB 2; Length 943;
Best Local Similarity 50.0%; Pred. No. 8.88e-01;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 595 RSRKCVPRKINGSN 608
:||||:|::|:|
QY 8 KSSKCVQKVEGSS 21

RESULT 10
ID Q50952 PRELIMINARY; PRT; 943 AA.
AC Q50952;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE LACTOFERRIN RECEPTOR PRECURSOR.
GN LBPA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FA19;
RC MEDLINE; 95347808.
RA BISWAS G.D., SPARLING P.F.;
RT "Characterization of lbpa, the structural gene for a lactoferrin
RT receptor in Neisseria gonorrhoeae.";
RL Infect. Immun. 63:2958-2967(1995).
CC -1- SIMILARITY: STRONG, TO N.MENINGITIDIS IRON-REGULATED OUTER
CC MEMBRANE PROTEIN A.
CC
DR EMBL; U15260; RAC13780.1; -.
DR PFAM; PF00593; TonB_boxC; 1.
KW Signal.
FT SIGNAL
FT CHAIN 1 24
FT CHAIN 25 943 LACTOFERRIN RECEPTOR.
SQ SEQUENCE 943 AA; 105669 MW; 4D8AF2C4 CRC32;

Query Match 41.8%; Score 59; DB 2; Length 943;
Best Local Similarity 50.0%; Pred. No. 8.88e-01;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 595 RSRKCVPRKINGSN 608
:||||:|::|:|
QY 8 KSSKCVQKVEGSS 21

RESULT 11
ID Q50969 PRELIMINARY; PRT; 205 AA.
AC Q50969;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PROTEIN TYROSINE PHOSPHATASE-LIKE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-SKELETAL MUSCLE;
MEDLINE; 96070766.

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RA WISHART M.J., DENU J.M., WILLIAMS J.A., DIXON J.E.;
RT "A single mutation converts a novel phosphotyrosine binding domain
RT into a dual-specificity phosphatase.";
RL J. Biol. Chem. 270:26782-26785(1995).
DR EMBL; U34973; AAA87036.1; -.
DR HSSP; P51452; 1VHR.
DR PFAM; PF00782; DSPC; 1.
SQ SEQUENCE 205 AA; 23683 MW; 7B70331A CRC32;

Query Match 41.1%; Score 58; DB 11; Length 205;
Best Local Similarity 25.0%; Pred. No. 1.44e+00;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 51 ILQKHGITHIICIRONIEAN 70
:|::|:|::|:|:|
QY 1 VIDHOGTKSSKCVQKVEGS 20

RESULT 12
ID Q60970 PRELIMINARY; PRT; 223 AA.
AC Q60970;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PROTEIN TYROSINE PHOSPHATASE-LIKE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-SKELETAL MUSCLE;
MEDLINE; 96070766.
RA WISHART M.J., DENU J.M., WILLIAMS J.A., DIXON J.E.;
RT "A single mutation converts a novel phosphotyrosine binding domain
RT into a dual-specificity phosphatase.";
RL J. Biol. Chem. 270:26782-26785(1995).
DR EMBL; U34973; AAA87037.1; -.
DR HSSP; P51452; 1VHR.
DR PFAM; PF00782; DSPC; 1.
SQ SEQUENCE 223 AA; 25416 MW; 7D7F6D83 CRC32;

Query Match 41.1%; Score 58; DB 11; Length 223;
Best Local Similarity 25.0%; Pred. No. 1.44e+00;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 51 ILQKHGITHIICIRONIEAN 70
:|::|:|::|:|:|
QY 1 VIDHOGTKSSKCVQKVEGS 20

RESULT 13
ID P71852 PRELIMINARY; PRT; 259 AA.
AC P71852;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE HYPOTHETICAL 26.8 KD PROTEIN.
GN MTCY03C7.07.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA SKELTON J., CHURCHER C.M.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

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 WISE (TM)

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MSrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:17:17 2000; Maspar time 2.98 seconds

Tabular output not generated. 166,869 Million cell updates/sec

Title: >US-08-487-283A-1
 Description: (1-21) from US08487283A.pep
 Perfect Score: 141
 Sequence: 1 VIDHOGTKSSKCVKRVKSS 21

Scoring table: PAM 150
 Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq36
 1:geneseqp

Statistics: Mean 18.949; Variance 55.942; scale 0.339

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	141	100.0	21	R77605	Pro-C5 polypeptide KSS	1.94e-09
2	141	100.0	1676	R77604	Pro-C5 polypeptide.	1.94e-09
3	57	40.4	117	Y07037	Breast cancer associat	3.93e+01
4	55	39.0	264	R22271	CSHase.	6.46e+01
5	54	38.3	249	W84049	Rice OsmA57 protein 1	8.26e+01
6	54	38.3	1732	W69487	Haemagglutinin protein	8.26e+01
7	54	38.3	1732	W24787	Prk antigenic protein	8.26e+01
8	54	38.3	1732	R96029	P. gingivalis porphyrin	8.26e+01
9	54	38.3	3163	R94347	Hepatitis GB virus (HG	8.26e+01
10	53	37.6	589	R14327	Mouse epithelin precu	1.05e+02
11	53	37.6	589	W85474	Mouse GP88 autocrine g	1.05e+02
12	53	37.6	652	R88124	Tobacco mosaic virus r	1.05e+02
13	53	37.6	1009	R26206	Type B human platelet-	1.05e+02
14	53	37.6	1089	R08267	Platelet derived growt	1.05e+02
15	53	37.6	1089	R06910	Alpha type PDGF recept	1.05e+02
16	53	37.6	1196	W04326	Rat perlin.	1.05e+02
17	52	36.9	14	W85479	Mouse GP88 autocrine g	1.34e+02
18	52	36.9	99	W54466	Mouse novel secreted p	1.34e+02
19	52	36.9	99	W5762	Human HDCA protein.	1.34e+02
20	52	36.9	186	W40824	Mycobacterium tubercul	1.34e+02
21	52	36.9	248	W84050	Rice OsmA58 protein 1	1.34e+02
22	52	36.9	354	R33439	Ornithine cyclodextrina	1.34e+02
23	52	36.9	455	W76439	Human p33 regulated pr	1.34e+02

24	52	36.9	593	1	W62835	2ea mays antimicrobial	1.34e+02
25	51	36.2	511	1	W78475	Autographa californica	1.71e+02
26	51	36.2	530	1	W78476	Baculovirus ISP protei	1.71e+02
27	51	36.2	589	1	R14325	Rat epithelin precursor	1.71e+02
28	51	36.2	637	1	W64388	A. thaliana SGT protei	1.71e+02
29	51	36.2	674	1	W64389	A. thaliana protein co	1.71e+02
30	51	36.2	707	1	W36064	Rat neurodap 1 protein	1.71e+02
31	51	36.2	730	1	Y00191	Enterococcus faecalis	1.71e+02
32	51	36.2	764	1	Y00190	Enterococcus faecalis	1.71e+02
33	51	36.2	914	1	R15785	B. thuringiensis toxin/	1.71e+02
34	51	36.2	956	1	R15784	B. thuringiensis toxin/	1.71e+02
35	51	36.2	986	1	R25141	UAK2.	1.71e+02
36	51	36.2	1100	1	R15783	B. thuringiensis toxin/	1.71e+02
37	51	36.2	1129	1	R70830	Murine JAK2 kinase.	1.71e+02
38	51	36.2	1144	1	R88122	Tobacco mosaic virus r	1.71e+02
39	51	36.2	1144	1	R88123	Tobacco mosaic virus r	1.71e+02
40	51	36.2	1588	1	R46605	Malariat PTEM3 epitop	1.71e+02
41	51	36.2	1663	1	R46608	Plasmodium falciparum	1.71e+02
42	50	35.5	37	1	W98577	H. pylori GPO 37 prot	2.17e+02
43	50	35.5	422	1	W56275	Flavobacterium keratol	2.17e+02
44	50	35.5	446	1	W69563	Sugarbeet choline mono	2.17e+02
45	50	35.5	1047	1	W01535	Cellular homologue of	2.17e+02

ALIGNMENTS

RESULT	1
ID	R77605 standard; Protein: 21 AA.
AC	R77605;
DT	02-APR-1996 (first entry)
DE	Pro-C5 polypeptide KSSKC epitope.
KW	Complement C5; haemolysis; kidney; glomerulonephritis;
KW	monoclonal antibody; antiinflammatory; antibody engineering;
KW	humanised antibody; KSSKC epitope.
OS	Homo sapiens.
PN	W09529697-A1.
PD	09-NOV-1995.
PF	01-MAY-1995: U05688.
PR	02-MAY-1994; US-236208.
PA	(ALEX-) ALEXION PHARM INC.
PI	Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
PI	Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI	Wang Y, Wilkins JA;
DR	WPI: 95-392923/50.
PT	Treating glomerulonephritis with antibody against complement C5
PT	Component - to inhibit complement induced cell lysis
PS	Example 13; Page 81; 181pp; English.
CC	The CDNA sequence of the complement C5 gene transcript predicts a
CC	secreted pro-C5 precursor of 1676 amino acids (R77604). C5 is a
CC	beta-globulin heterodimer thought to play a role in the pathogenesis
CC	of glomerulonephritis (GN). Cleavage of the C5 alpha-chain
CC	by a convertase enzyme generates anaphylatoxic C5a. Monoclonal
CC	and humanised recombinant antibodies that recognise the alpha-chain
CC	KSSKC epitope (R77605) block C5a generation, thereby reducing
CC	glomerular inflammation and kidney dysfunction associated with GN.
SO	Sequence 21 AA;
Query Match	100.0%; Score 141; DB 1; Length 21;
Best Local Similarity	100.0%; Pred. No. 1.94e-09;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 VIDHOGTKSSKCVKRVKSS 21
OY	1 VIDHOGTKSSKCVKRVKSS 21
RESULT	2
ID	R77604 standard; Protein: 1676 AA.
AC	R77604;
DT	15-MAR-1996 (first entry)
DE	Pro-C5 polypeptide.
KW	Complement C5; haemolysis; kidney; glomerulonephritis;
KW	monoclonal antibody; antiinflammatory; antibody engineering;


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KW humanised antibody.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..18 /label= Sig_peptide
FT protein 19..673
FT cleavage_site 673..674 /label= Beta-chain
FT cleavage_site 677..678
FT peptide 674..677 label= Cleavage_peptide
FT protein 678..1676 /label= Alpha-chain
FT /note= "amino acids 872-892 (854-874 of
the mature protein) comprise the KSSKS
epitope"
FT peptide 678..751 /label= c5a
FT cleavage_site 751..752
FT modified_site 911 /label= Convertase_cleavage_site
FT modified_site 1115 /label= N-glycosylation_site
FT modified_site 1630 /label= N-glycosylation_site
FT modified_site 1630 /label= N-glycosylation_site
FN WO9529697-A1.
PD 09-NOV-1995.
PF 01-MAY-1995; 005688.
PR 02-MAY-1994; US-236208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
PI WPI; 95-392923/50.
DR
PT Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS Example 13; Page 82-92; 181pp; English.
CC The cDNA sequence of the complement C5 gene transcript predicts a
CC secreted pro-C5 precursor of 1676 amino acids (R77604). C5 is a
CC beta-globulin heterodimer thought to play a role in the pathogenesis
CC of glomerulonephritis (GN). Cleavage of the C5 alpha-chain
CC by a convertase enzyme generates anaphylatoxin C5a. Monoclonal
CC and humanised recombinant antibodies that recognise the alpha-chain
CC KSSKC epitope (R77605) block C5a generation, thereby reducing
CC glomerular inflammation and kidney dysfunction associated with GN.
CC Sequence 1676 AA;
SQ
Query Match 100.0%; Score 141; DB 1; Length 1676;
Best Local Similarity 100.0%; Pred. No. 1.94e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 872 VIDHGTGKSSKCVQRKVEGSS 892
|VIDHGTGKSSKCVQRKVEGSS 21
QY

RESULT 3
ID Y07037 standard; Protein; 117 AA.
AC Y07037;
DT 02-JUL-1999 (first entry)
DE Breast cancer associated antigen precursor sequence.
KW Cancer associated antigen; diagnosis; research; treatment; human;
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW prostate cancer.
OS Homo sapiens.
PN WO9904265-A2.
PD 28-JAN-1999.
PF 15-JUL-1998; U14679.
PR 22-JUN-1998; US-1023322.
PR 17-JUL-1997; US-896164.
PR 10-OCT-1997; US-061599.
PR 10-OCT-1997; US-061765.

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PR 10-OCT-1997; US-948705.
PR 11-OCT-1997; GB-021697.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Chen Y, Gout I, Gure A, Ohare M, Obata Y, Old LJ,
PI Pfeundschnuh M, Sahin U, Scanlan MJ, Stockert E,
PI Tureci O;
PI WPI; 99-132448/11.
DR New isolated cancer associated nucleic acids and polypeptides -
PT isolated using sera from cancer patients, used to develop products
PT for the diagnosis, monitoring or treatment of cancers
PT Disclosure; Page 422; 787pp; English.
PS The invention relates to a method for diagnosing a disorder characterised
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically
CC binds to the NAM, an expression product or a fragment of an expression
CC product complexed with an HLA molecule; and (b) determining the
CC interaction between the agent and the NAM or the expression product as a
CC determination of the disorder. The products and methods can be used in
CC the diagnosis, monitoring, research, or treatment of conditions
CC characterised by the expression of various cancer associated antigens.
CC The invention provides nucleic acid sequences and encoded polypeptides
CC which are cancer associated antigen precursors expressed in human breast
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
CC lung cancer.
SQ Sequence 117 AA;

Query Match 40.4%; Score 57; DB 1; Length 117;
Best Local Similarity 41.7%; Pred. No. 3.93e-01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 80 GSMCAKCVEDRI 91
|:::|||||:::
QY 6 GTRSKCKVRQKV 17

RESULT 4
ID R22271 standard; Protein; 264 AA.
AC R22271;
DT 30-JUL-1992 (first entry)
DE CSHase.
KW N-carbamoyl-sarcosine amidohydrolase; CSH; assay; diagnosis;
KW creatinine.
OS Arthrobacter sp. DSM 2563.
PN Ep-476670-A.
PD 25-MAR-1992.
PF 19-SEP-1991; 115974.
PR 20-SEP-1990; DE-029844.
PA (BOFF) BOEHRINGER MANNHEIM GMBH.
PI Burtcher H, Schumacher G;
PI WPI; 92-098378/13.
DR N-PSDB; Q22713.
PT Recombinant DNA encoding N-carbamoyl-sarcosine-amidohydrolase -
PT useful in clinical assay of creatinine, and vectors providing
PT efficient expression in E.coli
PS Claim 9; Page 9 + 7; 12pp; German.
CC The sequence encoding CSHase is useful in assay of creatinine
CC (for diagnosis of kidney disease). It can now be prep. more
CC simply than by known methods which involve culture of Arthrobacter
CC on complex media.
SQ Sequence 264 AA;

Query Match 39.0%; Score 55; DB 1; Length 264;
Best Local Similarity 46.2%; Pred. No. 6.46e-01;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 171 GATACGVRHVE 183
|:::|||||:::
QY 6 GTRSKCKVRQKVE 18

RESULT 5
ID W84049 standard; Protein; 249 AA.

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[illegible]

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CC vaccines against periodontal disease.
SC Sequence 1732 AA;

Query Match      38.3%; Score 54; DB 1; Length 1732;
Best Local Similarity 31.6%; Pred. No. 8.26e+01;
Matches          6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db    1097 ITAKVRSFKAIRGRIQGT 1115
      | :|:| :| :|:|:
Oy    2 IDHOGTKSSKCVRKVEGS 20

RESULT 7
ID W24787 standard; Protein; 1732 AA.
AC W24787;
DT 25-NOV-1997 (first entry)
DE Ptk antigenic protein complex.
KW Periodontal disease; cell surface protein; thiol protease;
   endopeptidase; Ptk; Ptk48; Ptk39; Ptk15; Ptk44;
   haemagglutinin; adhesin; therapy; diagnosis; vaccine; antigen.
OS Porphyromonas gingivalis strain W50.
FH Key .location/Qualifiers
FE peptide 1..228
FT /label= Pro-pro-peptide
FT cleavage_site 228..229
FT protein 229..737
FT /label= Ptk48
FT /note= "48 kDa Lys-specific thiol protease"
FT cleavage_site 737..738
FT protein 738..1156
FT /label= Ptk39
FT /note= "39 kDa adhesin"
FT cleavage_site 1156..1157
FT protein 1157..1291
FT /label= Ptk15
FT /note= "15 kDa adhesin"
FT cleavage_site 1291..1292
FT protein 1292..1732
FT /label= Ptk44
FT /note= "44 kDa adhesin"

WO9716542-A1.
PD 09-MAY-1997.
PF 30-OCT-1996; AU0673.
PR 30-OCT-1995; AU-006275.
PA (UYME ) UNIV MELBOURNE.
PB (VTCE-) VICTORIAN DAIRY IND AUTHORITY.
PI Bhogal PS, Reynolds EC, Slakeski N;
DR WPI; 97-272112/24.
DR N-PSDB; T78851.
PT New antigenic protein complex from Porphyromonas gingivalis -
   comprising Arg- and Lys- specific thiol endo-peptidase(s), used in
   the detection, prevention and treatment of periodontal disease
   Example 1; Fig 9b; 68pp: English.
PC A Ptk-Ptk cell surface protein of Porphyromonas gingivalis (Pg)
   comprises a 300 kDa complex composed a 48 kDa lysine-specific
   thiol protease and 39, 15 and 44 kDa adhesins encoded by the ptk
   gene (T78851), and a 45 kDa arginine-specific thiol protease and
   44, 15, 17 and 27 kDa adhesins (see W24786) encoded by the ptk
   gene (T78850). A claimed antigenic complex comprises at least one
   multimeric protein complex of PtkR and Ptk each containing at
   least one adhesion domain, the complex having a mol.wt. of over 200
   kDa, and preferably comprises all 9 proteins of the PtkR-Ptk
   complex (see also W24780-85). It can be used in a claimed
   composition to elicit an immune response directed against Pg, and
   in a claimed method of reducing the prospect of Pg infection and/or
   severity of disease. Antibodies directed against the complex are
   claimed for use in treating Pg infection. Unlike whole Pg cells or
   other previously prepared antigens based on fimbriae or the
   capsule, the PtkR-Ptk complex or component parts are safe and
   effective antigens.
SC Sequence 1732 AA;
```

Best Local Similarity 31.6%; Pred. No. 8.26e+01;
Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1097 ITAKGVSRPKAIRIGIQT 1115

QY 2 IDHQGTKSKCVRKVEGS 20

RESULT 8

ID R96029 standard; Protein; 1732 AA.

AC R96029;

DT 04-SEP-1996 (first entry)

DE P. gingivalis porphyain.

OS Porphyain; haemagglutinin; periodontal disease; vaccine; antibody.

KW Porphyromonas gingivalis strain W12.

FT Key Location/Qualifiers

FT region 688..708

FT /note="Pro-Asn repeat region type 1"

FT region 887..952

FT /note="Pro-Asn repeat region type 2"

FT region 946..967

FT /note="Pro-Asn repeat region type 1"

FT region 985..1006

FT /note="Pro-Asn repeat region type 3"

FT region 1041..1100

FT /note="Pro-Asn repeat region type 4"

FT region 1341..1405

FT /note="Pro-Asn repeat region type 2"

FT region 1430..1451

FT /note="Pro-Asn repeat region type 3"

FT region 1488..1547

FT /note="Pro-Asn repeat region type 4"

FT region 1607..1650

FT /note="Pro-Asn repeat region type 2"

PN W09617936-A2.

PD 13-JUN-1996.

PF 11-DEC-1995; U16108.

PR 09-DEC-1994; US-353485.

PA (UABR-) UAB RES FOUND.

PA (UFL) UNIV FLORIDA.

PI Han N, Lantz M, Lepine G, Patti JM, Progulake-Fox A;

PI Tumwasorn S;

DR WPI: 96-287181/29.

DR N-PSDB: T30653.

PT Porphyromonas gingivalis genes and proteins - used in the detection

PT and vaccination against periodontal disease

PS Claim 5; Page 76-81; 153pp; English.

CC P. gingivalis W12 cysteine protease, porphyain (R96029), was

CC identified as the product of the prp gene (T30653) isolated from

CC P. gingivalis W12 genomic DNA. The porphyain shows homology to

CC the haemagglutinins (see also R96026-28 and R96030-33) of P.

CC gingivalis 318. It can be obtd. from transformed host cells and

CC used as a vaccine to protect humans or animals against periodontal

CC disease. Expression in Salmonella cells allows prodn. of a live

CC vaccine. The porphyain and haemagglutinins can also be used to

CC detect the presence of anti-P. gingivalis antibodies and to raise

CC monoclonal antibodies for diagnostic appln.

SQ Sequence 1732 AA;

Query Match

Best Local Similarity 38.3%; Score 54; DB 1; Length 1732;

Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1097 ITAKGVSRPKAIRIGIQT 1115

QY 2 IDHQGTKSKCVRKVEGS 20

RESULT 9

ID R94347 standard; Protein; 3163 AA.

AC R94347;

DT 02-JUL-1996 (first entry)

DE Hepatitis GB virus (HGBV) clone GB contig A protein prod.

KW Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine;
KW reagents; non-A; non-B; non-C; non-D; non-E; clone; GB contig A;
KW tamarin; infected plasma; lambda phase; cDNA library.

OS Hepatitis GB virus.

FT Key Location/Qualifiers

FT misc_difference 1..3163

FT /note="others correspond to degenerate or STOP

FT codons in T00129"

PN W09521922-A2.

PD 17-AUG-1995.

PF 14-FEB-1995; U02118.

PR 14-FEB-1994; US-196030.

PR 13-MAY-1994; US-242654.

PR 29-JUL-1994; US-283314.

PR 23-NOV-1994; US-344190.

PR 23-NOV-1994; US-344185.

PR 27-JAN-1995; US-344557.

PA (ABSO) ABBOTT LAB.

PI Buijk SL, Dawson GJ, Desai SM, Erker JC, Leary TP;

PI Muerthoff AS, Mushahwar IK, Pilot-Matias TJ, Schlauder GG;

PI Simons JN;

DR WPI: 95-293123/38.

DR N-PSDB; T00129.

PT Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful

PT for diagnosis and therapy of hepatitis GB virus

PS Example 9; Pages 401-414; 661pp; English.

CC Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV

CC infected tamarin plasma, using standard procedures, was used to

CC prepare a lambda phage HGBV cDNA library. Clones were rescued

CC from the lambda phage, searched against a sequence database and

CC found to be unique HGBV sequences. The clones were then used to

CC assemble the sequences T00129/30 (GB contig A and B) which encode

CC the proteins R94345-47 (the 3 possible coding strand reading

CC frames) and R82072, respectively. Reagents which comprise the HGBV

CC DNA, or its protein prods. can be used for the diagnosis, therapy

CC or in a vaccine to prevent HGBV infection.

SQ Sequence 3163 AA;

Query Match

Best Local Similarity 38.3%; Score 54; DB 1; Length 3163;

Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 528 VVDORPLKGCVCVRD 542

QY 1 VIDHQGTKSKCVRQ 15

RESULT 10

ID R14327 standard; Protein; 589 AA.

AC R14327;

DT 17-JAN-1992 (first entry)

DE Mouse epithelin precursor.

KW ET; growth regulation; inhibition; stimulation.

OS Mus musculus.

FT Key Location/Qualifiers

FT protein 1..589

FT /label= precursor

FT /note="claim 21, page 55"

FT 280..335

FT /label= Ep-1

FT /note="claim 22, page 55"

FT 205..261

FT /label= Ep-2

FT /note="claim 23, page 55"

FT 59..114

FT /label= Ep

FT /note="claim 24, page 55"

FT 123..179

FT /label= Ep

FT /note="claim 25, page 55"

FT 362..416

FT /label= Ep

FT /note="claim 26, page 56"

FT peptide 440. :495
 FT /label=EP
 FT /note="claim 27, page 56"
 FT peptide 515. :570
 FT /label=EP
 FT /note="claim 28, page 56"
 PN WO9115510-A.
 PD 17-OCT-1991.
 PF 03-APR-1991: US02321.
 PR 03-APR-1990: US-504508.
 PR 13-MAR-1991: US-083796.
 PA (BRIM) BRISTOL-MYERS SQUIB.
 PI Shoyab M, Plozman GD;
 DR N-PSDB: 014340.
 DR N-PSDB: 014340.
 PT New cysteine-rich growth modulating proteins, epithelins - useful as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
 PS Disclosure; Fig 23; 97pp; English.
 CC ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others.
 CC ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bioactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.
 CC See also 014338-40, 014952-53, R14328-9 and R15315-20.
 CC Sequence 589 AA;
 SQ

Query Match 37.6%; Score 53; DB 1; Length 589;
 Best Local Similarity 35.7%; Pred. No. 1.05e+02;
 Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 560 HCSARCTCLRRKI 573
 | : : : : | : | :
 QY 4 HOGTKSKCVROKV 17

RESULT 11
 ID W85474 standard; Protein: 589 AA.
 AC W85474;
 DT 15-MAR-1999 (first entry)
 DE Mouse GP88 autocrine growth factor.
 KW GP88; granulatin; epithelin; mouse; growth factor; autocrine; tumour;
 KM cancer; viral infection; antagonist; therapy; diagnosis.
 OS Mus sp.
 FH key
 PT Location/Qualifiers
 FT Misc-difference 8
 FT /note="encoded by CTG"
 FT Misc-difference 54
 FT /note="encoded by AGC"
 FT Misc-difference 377
 FT /note="encoded by TGA"
 FT peptide 208. :219
 FT /note="P12T peptide used to raise antibody"
 FT peptide 344. :362
 FT /note="K19T peptide, used to raise antibody"
 FT peptide 562. :575
 FT /note="S14R peptide, used to raise antibody"
 PN WO9852607-A1.
 PD 26-NOV-1998.
 PF 22-MAY-1998: U10555.
 PR 16-DEC-1997: US-991862.
 PR 23-MAY-1997: US-863079.
 PA (SERR/) SERRERO G.
 PI Serrero G;
 DR WPI: 99-045276/04.
 DR N-PSDB: V82824.
 PT Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease
 PS Example 5; Fig 8A-D; 86pp; English.
 CC This is the amino acid sequence of murine GP88, an 88 kDa glycoprotein autocrine growth factor and epithelin/granulin

CC precursor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. Inhibition of GP88 expression or action in the tumorigenic cells results in an inhibition of the tumorigenic properties of the overproducing cells. Murine GP88 cDNA (see V82824) was obtained from the highly tumorigenic PC cell line. Antagonists to GP88 are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Fragments of GP88 are used to raise specific antibodies (used as antagonists, as diagnostic reagents and for delivering toxins or other compounds to GP88-expressing cells) and to screen for antibodies. Methods are provided for diagnosing disease, or determining susceptibility to disease, resulting from altered GP88 activity.
 CC Sequence 589 AA;
 SQ

Query Match 37.6%; Score 53; DB 1; Length 589;
 Best Local Similarity 35.7%; Pred. No. 1.05e+02;
 Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 560 HCSARCTCLRRKI 573
 | : : : : | : | :
 QY 4 HOGTKSKCVROKV 17

RESULT 12
 ID R88124 standard; Protein: 652 AA.
 AC R88124;
 DT 28-MAR-1996 (first entry)
 DE Tobacco mosaic virus resistance N gene truncated protein.
 KW Tobacco mosaic virus resistance; TMV; N gene; Solanaceae;
 KM crop improvement; transgenic plant; crop improvement.
 OS Nicotiana glauca.
 PN WO9535024-A1.
 PD 28-DEC-1995.
 PF 16-JUN-1995: U07754.
 PR 17-JUN-1994: US-261663.
 PA (RESC) UNIV CALIFORNIA.
 PA (USDA) US SEC OF AGRIC.
 PI Baker BJ, Whitlam SA;
 DR WPI: 96-058144/06.
 DR N-PSDB: T09342.
 PT Plant virus resistance gene N sequences from tobacco - useful for generating transgenic Solanaceous plants resistant to Tobacco Mosaic Virus
 FT Virus
 PS Claim 28; Page 75-79; 98pp; English.
 CC The Nicotiana glauca N gene truncated protein (R88124) mediates resistance to tobacco mosaic virus (TMV). A cDNA clone (T09342) coding for the protein was obtd. from a N. glauca leaf cDNA library by transposon tagging. DNA sequences encoding the protein can be used to generate transgenic plants, esp. Solanaceae, resistant to TMV.
 CC Sequence 652 AA;
 SQ

Query Match 37.6%; Score 53; DB 1; Length 652;
 Best Local Similarity 31.3%; Pred. No. 1.05e+02;
 Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 156 DNRKTDADCIROYD 171
 | : : : : | : | :
 QY 3 DHOGTKSKCVROKVE 18

RESULT 13
 ID R26206 standard; Protein: 1009 AA.
 AC R26206;
 DT 09-FEB-1993 (first entry)
 DE Type B human platelet-derived growth factor receptor.
 KW PDGFR; PDGFR-R; mesenchyme; tyrosine kinase; ligand binding region.
 OS Homo sapiens.
 FH key
 PT Location/Qualifiers
 FT peptide 1. :23

FT protein /label= signal_peptide
 FT 24..1009
 FT /label= Mature_PDGFR-A
 PN WO9213867-A.
 PD 20-AUG-1992.
 PF 28-JAN-1992; U00730.
 PR 31-JAN-1991; US-650793.
 PA (CORT-) COR THERAPEUTICS INC.
 PI Escobedo JA, Fretto LJ, Giese NA, Tomlinson JE, Williams LT;
 PI Wolf D;
 DR WPI; 92-299970/36.
 DR N-PSDB; Q27451.
 PT Platelet derived growth factor receptor (PDGFR-R) poly:peptide(s)
 PT - useful as therapeutic and diagnostic agents e.g. for assaying
 PT PDGFR activity in sample
 PS Disclosure; Page 90; 109pp; English.
 CC The sequence given is one allele of type A human platelet-derived
 CC growth factor (PDGFR) receptor (PDGFR-R). This receptor is typically
 CC found on cells of mesenchymal origin. It acts while in the form of
 CC two transmembrane glycoproteins, each of which is about 180 kD.
 CC This receptor has three major regions. The first is a transmembrane
 CC region, which spans the membrane once, separating the regions of the
 CC receptor exterior to the cell from those interior to the cell. The
 CC second region is an extracellular region which contains the domains
 CC which bind the PDGF. The third region is an intracellular region
 CC which possesses a tyrosine kinase activity. This tyrosine kinase
 CC domain is notable in having an insert of approx. 100 amino acids,
 CC as compared with most other receptor tyrosine kinase domains which
 CC are contiguous or have shorter insert sequences. Fragments of this
 CC sequence between 8 and 400 amino acids comprising one or more PDGF
 CC ligand binding region from the extracellular domain may be used to
 CC bind a PDGF ligand.
 CC Sequence 1009 AA;
 SQ

Query Match 37.6%; Score 53; DB 1; Length 1009;
 Best Local Similarity 38.1%; Pred. No. 1.05e+02;
 Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 381 VDDHGGTGGGTGTCRTAGTGP 401
 | | | : : : | | | : : :
 QY 1 VIDHGTGKSKCKVRQKVEGSS 21

RESULT 14
 ID R08267; standard; protein; 1089 AA.
 AC R08267;
 DT 07-MAR-1991 (first entry)
 DE Platelet derived growth factor (PDGFR) receptor protein.
 KW Atherosclerosis; fibrotic diseases.
 OS Homo sapiens.
 PN WO9014425-A.
 PD 29-NOV-1990.
 PF 21-MAY-1990; U02849.
 PR 22-MAY-1989; US-355018.
 PA (Zymo-) ZYMOGENETICS INC.
 PI Kelly JD, Murray MJ;
 DR WPI; 90-375992/50.
 DR N-PSDB; Q06869.
 PT DNA encoding platelet-derived growth factor - used to transform
 PT cells for culturing to detect PDG agonists and antagonists
 PS Claim 1; Fig 1; 30pp; English.
 CC Gene product may be expressed from a transformed cell. It has
 CC utility in detection of PDGF agonist and antagonist analogues, binding
 CC AA, AB and BB isoforms. PDGF agonists may be used to enhance wound
 CC healing, and antagonists may be used to block the effects of PDGF
 CC eg. in treatment of atherosclerosis or fibrotic diseases.
 CC Sequence 1089 AA;
 SQ

Query Match 37.6%; Score 53; DB 1; Length 1089;
 Best Local Similarity 38.1%; Pred. No. 1.05e+02;
 Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db .421 VDDHGGTGGGTGTCRTAGTGP 441

QY 1 VIDHGTGKSKCKVRQKVEGSS 21
 | | | : : : | | | : : :
 RESULT 15
 ID R06910 standard; protein; 1089 AA.
 AC R06910;
 DT 16-JAN-1991 (first entry)
 DE Alpha type PDGF receptor deduced from TR4 CDNA clone.
 KW Platelet derived growth factor; T11.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..23
 FT /label=signal peptide
 FT domain 24..524
 FT /label=ligand binding domain
 FT domain 525..548
 FT /label=transmembrane region
 FT domain 549..599
 FT /label=juxtamembrane domain
 FT binding_site 600..627
 FT /label=ATP binding site
 FT modified_site 849
 FT /label=tyrosine autophosphorylation site
 FT modified_site 42..44
 FT /label=N-glycos_site
 FT modified_site 76..78
 FT /label=N-glycos_site
 FT modified_site 103..105
 FT /label=N-glycos_site
 FT modified_site 179..181
 FT /label=N-glycos_site
 FT modified_site 353..355
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 FT modified_site 359..361
 FT /label=N-glycos_site
 FT modified_site 458..460
 FT /label=N-glycos_site
 FT modified_site 468..470
 FT /label=N-glycos_site
 PN WO9010013-A.
 PD 07-SEP-1990.
 PF 08-FEB-1990; U00617.
 PR 09-FEB-1989; US-308282.
 PA (USDC) US SEC OF COMMERCE.
 PI Matsui T, Aaronson SA, Pierce JH;
 DR N-PSDB; Q05989.
 PT Type alpha platelet-derived growth factor receptor gene - useful
 PT for transforming cells to express novel protein receptor and also
 PT susceptible to genetic engineering.
 PS Claim 7; Fig 3; 64pp; English.
 CC The TR4 clone is the largest cDNA clone related to the T11 genomic
 CC clone, isolated from a library prepd. from human thymus DNA. The
 CC T4 CDNA clone was isolated from a M426 human embryo fibroblast
 CC cDNA library. The coding region can be introduced into the pSV2
 CC gpt vector with a simian sarcoma virus LTR as a promoter and
 CC expressed in a host. The resulting protein is a novel PDGF
 CC receptor designated type alpha (the known receptor is designated
 CC type beta). The polypeptide has a calculated molecular mass of 120
 CC kD and has all the characteristics of a membrane spanning tyrosine
 CC kinase receptor. The extracellular region comprises a hydrophobic
 CC signal peptide and a ligand binding domain which has structural
 CC homology with the PDGF-R/CSF1-R subfamily. Ten Cys residues are
 CC spaced at the same positions as in other receptors of the sub-
 CC family and eight potential N-linked glycosylation sites are also
 CC present. A hydrophobic segment spans the membrane and the cyto-
 CC plasmic region comprises a juxtamembrane region, a tyrosine kinase
 CC region split into TK1 and TK2 by a hydrophilic interkinase region
 CC and a hydrophilic C-terminal tail. The TK region includes the
 CC consensus ATP binding sequence (G-X-G-X-G..K) and a tyrosine
 CC autophosphorylation site homologous to that of pp60(v-src).
 CC Sequence 1089 AA;
 SQ

Query Match 37.6%; Score 53; DB 1; Length 1089;
Best Local Similarity 38.1%; Pred. No. 1.05e+02;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

DB 421 VDDHGSTGGQTVRCTAETP 441

QY 1 VIDHGTSSKCVRQKVEGSS 21

Search completed: Wed Sep 6 08:17:28 2000
Job time : 11 secs.

MORSE
(TM)

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Msrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:17:46 2000; Maspar time 2.27 Seconds

Tabular output not generated. 141.637 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (1-21) from US08487283A.pep
Perfect Score: 141
Sequence: 1 VIDHGTSSKCVROKVEGSS 21

Scoring table: PAM 150
Gap 15

Searched: 152433 seqs, 15329240 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 17.928; Variance 54.211; scale 0.331

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
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2	59	41.8	944	2	US-08-867- Sequence 24, Applicat	1.44e+01
3	58	41.1	24	2	US-08-827- Sequence 127, Applicat	1.85e+01
4	58	41.1	24	1	US-08-484- Sequence 127, Applicat	1.85e+01
5	58	41.1	24	2	US-08-484- Sequence 127, Applicat	1.85e+01
6	55	39.0	264	1	US-08-107- Sequence 2, Applicatio	3.90e+01
7	54	38.3	249	2	US-08-867- Sequence 15, Applicati	4.99e+01
8	54	38.3	1732	2	US-08-353- Sequence 10, Applicati	4.99e+01
9	54	38.3	1732	2	US-08-570- Sequence 6, Applicatio	6.38e+01
10	53	37.6	589	2	US-08-431- Sequence 6, Applicatio	6.38e+01
11	53	37.6	589	2	PCT-US91-0 Sequence 6, Applicatio	6.38e+01
12	53	37.6	589	2	US-08-429- Sequence 6, Applicatio	6.38e+01
13	53	37.6	589	1	US-07-668- Sequence 6, Applicatio	6.38e+01
14	53	37.6	652	4	PCT-US95-0 Sequence 6, Applicatio	6.38e+01
15	53	37.6	652	1	US-08-261- Sequence 6, Applicatio	6.38e+01
16	53	37.6	1089	3	US-08-462- Sequence 2, Applicatio	6.38e+01
17	53	37.6	1089	4	PCT-US92-0 Sequence 4, Applicatio	6.38e+01
18	53	37.6	1089	4	US-08-475- Sequence 36, Applicati	6.38e+01
19	53	37.6	1089	2	US-08-867- Sequence 36, Applicati	6.38e+01
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21	53	37.6	1089	3	US-08-460- Sequence 4, Applicatio	6.38e+01
22	53	37.6	1089	1	US-08-168- Sequence 4, Applicatio	6.38e+01
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24	53	37.6	1089	1	US-08-477- Sequence 36, Applicati	6.38e+01
25	53	37.6	1089	1	US-08-180- Sequence 36, Applicati	6.38e+01
26	53	37.6	1143	2	US-08-310- Sequence 108, Applicat	6.38e+01
27	53	37.6	1143	4	PCT-US95-0 Sequence 108, Applicat	6.38e+01
28	53	37.6	1144	4	PCT-US95-0 Sequence 2, Applicatio	6.38e+01
29	53	37.6	1144	4	PCT-US95-0 Sequence 2, Applicatio	6.38e+01
30	53	37.6	1144	1	US-08-261- Sequence 2, Applicatio	6.38e+01
31	53	37.6	1144	1	US-08-261- Sequence 4, Applicatio	6.38e+01
32	52	36.9	99	2	US-08-795- Sequence 1, Applicatio	8.13e+01
33	52	36.9	186	2	US-08-655- Sequence 15, Applicati	8.13e+01
34	52	36.9	186	2	US-08-655- Sequence 2, Applicatio	8.13e+01
35	52	36.9	248	2	US-08-667- Sequence 17, Applicati	8.13e+01
36	52	36.9	317	2	US-08-477- Sequence 4, Applicatio	8.13e+01
37	51	36.2	530	3	US-09-105- Sequence 2, Applicatio	1.04e+02
38	51	36.2	589	2	US-08-431- Sequence 2, Applicatio	1.04e+02
39	51	36.2	589	2	US-08-429- Sequence 2, Applicatio	1.04e+02
40	51	36.2	993	1	US-08-446- Sequence 25, Applicati	1.04e+02
41	51	36.2	1129	4	PCT-US95-1 Sequence 2, Applicatio	1.04e+02
42	51	36.2	1129	1	US-08-097- Sequence 9, Applicatio	1.04e+02
43	51	36.2	1129	1	US-08-357- Sequence 6, Applicatio	1.04e+02
44	51	36.2	1129	2	US-09-003- Sequence 6, Applicatio	1.04e+02
45	51	36.2	1663	4	PCT-US93-0 Sequence 16, Applicati	1.04e+02

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	944 AA.
ID	US-08-867-941-23			
AC	xxxxxx			
XX				
DT				
XX				
DE				
XX				

Sequence 23, Application US/08867941

Sequence 23, Application US/08867941

Patent No. 5977337

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M

APPLICANT: Du, Run-Pan

APPLICANT: Wang, Qiljun

APPLICANT: Yang, Yan-Ping

APPLICANT: Kiehn, Michel H

TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Slim & McBurney

STREET: 6th Floor, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/867,941

FILING DATE: 03-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 944 amino acids

TYPE: amino acid

STRANDEDNESS: single

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CC      TOPOLOGY: linear
SQ      SEQUENCE 944 AA; 105523 MW; 4449713 CN;

Query Match      41.8%; Score 59; DB 2; Length 944;
Best Local Similarity 50.0%; Pred. No. 1.44e+01;
Matches      7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db      596 RSRKCVPRKINGSN 609
QY      8 KSSKCVQKVEGSS 21

RESULT      2
ID      US-08-867-941-24      STANDARD;      PRT;      944 AA.
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AC      xxxxxx
DT
DE
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XX
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XX      Sequence 24, Application US/08867941
XX
XX      Sequence 24, Application US/08867941
CC      Patent No. 5977337
CC      GENERAL INFORMATION:
CC      APPLICANT: Loomore, Sheena M
CC      APPLICANT: Du, Run-Pan
CC      APPLICANT: Wang, Quljun
CC      APPLICANT: Yang, Yan-Ping
CC      APPLICANT: Klein, Michel H
CC      TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
CC      NUMBER OF SEQUENCES: 67
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Sim & McBurney
CC      STREET: 6th Floor, 330 University Avenue
CC      CITY: Toronto
CC      STATE: Ontario
CC      COUNTRY: Canada
CC      ZIP: M5G 1R7
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/867,941
CC      FILING DATE: 03-JUN-1997
CC      CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Stewart, Michael I
CC      REGISTRATION NUMBER: 24,973
CC      REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (416) 595-1155
CC      TELEFAX: (416) 595-1163
CC      INFORMATION FOR SEQ ID NO: 24:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 944 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
SQ      SEQUENCE 944 AA; 105738 MW; 4434179 CN;

Query Match      41.8%; Score 59; DB 2; Length 944;
Best Local Similarity 50.0%; Pred. No. 1.44e+01;
Matches      7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db      596 RSRKCVPRKINGSN 609
QY      8 KSSKCVQKVEGSS 21

RESULT      3
ID      US-08-827-570-127      STANDARD;      PRT;      24 AA.
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XX      Sequence 127, Application US/08827570
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XX      Sequence 127, Application US/08827570
CC      Patent No. 5986047
CC      GENERAL INFORMATION:
CC      APPLICANT: Wrighton, Nicholas C.
CC      APPLICANT: Dower, William J.
CC      APPLICANT: Chang, Ray S.
CC      APPLICANT: Kashyap, Arun K.
CC      APPLICANT: Jolliffe, Linda K.
CC      APPLICANT: Johnson, Dana
CC      APPLICANT: Mulcahy, Linda
CC      TITLE OF INVENTION: Compounds and Peptides That Bind to the
CC      TITLE OF INVENTION: Erythropoietin Receptor
CC      NUMBER OF SEQUENCES: 259
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Townsend and Townsend and Crew
CC      STREET: One Market Plaza, Steuart Street Tower
CC      CITY: San Francisco
CC      STATE: California
CC      COUNTRY: USA
CC      ZIP: 94105-1492
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/827,570
CC      FILING DATE:
CC      CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/484,635
CC      FILING DATE: 07-JUN-1995
CC      APPLICATION NUMBER: US 08/155,940
CC      FILING DATE: 19-NOV-1993
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Garrett-Wackowski, Eugenia
CC      REGISTRATION NUMBER: 37,330
CC      REFERENCE/DOCKET NUMBER: 16528A-43-1-1
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (415) 543-9600
CC      TELEFAX: (415) 543-5043
CC      INFORMATION FOR SEQ ID NO: 127:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 24 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS:
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: peptide
SQ      SEQUENCE 24 AA; 2547 MW; 2814 CN;

Query Match      41.1%; Score 58; DB 2; Length 24;
Best Local Similarity 46.7%; Pred. No. 1.85e+01;
Matches      7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db      10 QGPKTWPCVRRRLGG 24
QY      5 QGKSKCVQKRVQVEG 19

RESULT      4
ID      US-08-484-635-127      STANDARD;      PRT;      24 AA.
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AC      xxxxxx
DT
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DE Sequence 127, Application US/08484635
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CC Sequence 127, Application US/08484635
CC Patent No. 5773569
CC GENERAL INFORMATION:
CC APPLICANT: Wrighton, Nicholas C.
CC APPLICANT: Dower, William J.
CC APPLICANT: Chang, Ray S.
CC APPLICANT: Kashyap, Atun K.
CC APPLICANT: Jolliffe, Linda K.
CC APPLICANT: Johnson, Dana
CC APPLICANT: Mulcahy, Linda
CC TITLE OF INVENTION: Compounds and Peptides That Bind to the
CC TYPE OF INVENTION: Erythropoietin Receptor
CC NUMBER OF SEQUENCES: 259
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Crew
CC STREET: One Market Plaza, Stewart Street Tower
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105-1492
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/484,635
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/155,940
CC FILING DATE: 19-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Garrett-Wackowski, Eugenia
CC REGISTRATION NUMBER: 37,330
CC REFERENCE/DOCKET NUMBER: 16528A-43-1-1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 127:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 24 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 24 AA: 2547 MW: 2814 CN:
SQ
Query Match 41.1%; Score 58; DB 1; Length 24;
Best Local Similarity 46.7%; Pred.NO. 1.85e+01;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0.
Db 10 GQKTPCVRRRLG 24
QY 5 GQTKSSKCVRKVEG 19
RESULT 5 STANDARD; PRT; 24 AA.
XX US-08-484-631-127
XX AC xxxxxx
XX DT
XX
DE Sequence 127, Application US/08484631
CC Sequence 127, Application US/08484631
CC Patent No. 5830851
CC GENERAL INFORMATION:
CC APPLICANT: Wrighton, Nicholas C.
CC APPLICANT: Dower, William J.
CC

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CC APPLICANT: Chang, Ray S.
CC APPLICANT: Kashyap, Arun K.
CC APPLICANT: Jolliffe, Linda K.
CC APPLICANT: Johnson, Dana
CC APPLICANT: Mulcahy, Linda
CC TITLE OF INVENTION: Compounds and Peptides That Bind to the
CC TITLE OF INVENTION: Erythropoietin Receptor
CC NUMBER OF SEQUENCES: 259
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew
CC STREET: One Market Plaza, Steuart Street Tower
CC City: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105-1492
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/484,631
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/155,940
CC FILING DATE: 19-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Garrett-Wackowski, Eugenia
CC REGISTRATION NUMBER: 37,330
CC REFERENCE/DOCKET NUMBER: 16528A-43-1-2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC INFORMATION FOR SEQ ID NO: 127:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 24 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 24 AA: 2547 MW; 2814 CN;
Db 10 GGRKTPCVRRRLGG 24
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Oy 5 GGRSSKCVFQKEG 19
RESULT 6
ID US-08-107-042-2 STANDARD: PRT; 264 AA.
XX xxxxxx
DE Sequence 2, Application US/08107042
CC Sequence 2, Application US/08107042
CC Patent No. 5416014
CC GENERAL INFORMATION:
CC APPLICANT: Butscher, Helmut
CC APPLICANT: Schumacher, Gunther
CC TITLE OF INVENTION: CLONED N-CARBAMOYL SARCOSINE
CC TITLE OF INVENTION: AMIDOHYDROLASE
CC NUMBER OF SEQUENCES: 3
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Armstrong, Nikolaïd, Marmelstein, Kubovcik &
CC ADDRESSEE: MurRAY
CC STREET: 1725 K Street N.W., Suite 1000

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CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/241,640
CC FILING DATE: 08-SEP-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Whitlock, Ted W.
CC REGISTRATION NUMBER: 36,965
CC REFERENCE/DOCKET NUMBER: UF15.C2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (904) 375-8100
CC TELEFAX: (904) 372-5800
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1732 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1732 AA; 187874 MW; 16128552 CN;
SO

Query Match 38.3%; Score 54; DB 2; Length 1732;
Best Local Similarity 31.6%; Pred. No. 4.99e+01;
Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1097 ITAKGVSPKAIKRGRIQGT 1115
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QY 2 IDHGTGKSKVCVRQKVEGS 20

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ID US-08-570-311-10 STANDARD; PRT: 1732 AA.
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Sequence 10, Application US/08570311
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Sequence 10, Application US/08570311
CC Patent No. 5824791
CC GENERAL INFORMATION:
CC APPLICANT: Proguiske-Fox, Ann
CC APPLICANT: Tumwasorn, Somying
CC APPLICANT: Lepine, Guylaine
CC APPLICANT: Han, Naiming
CC APPLICANT: Lantz, Marilyn
CC APPLICANT: Patti, Joseph
CC TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
CC TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Ted W. Whitlock
CC STREET: 2421 N.W. 41st Street, Suite A-1
CC CITY: Gainesville
CC STATE: FL
CC COUNTRY: USA
CC ZIP: 32606
CC COMPUTER READABLE FORM:
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,311
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/353,485
CC FILING DATE: 09-DEC-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/647,119
CC FILING DATE: 25-JAN-1991
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/241,640
CC FILING DATE: 08-SEP-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Whitlock, Ted W.
CC REGISTRATION NUMBER: 36,965
CC REFERENCE/DOCKET NUMBER: UF15.C3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (904) 375-8100
CC TELEFAX: (904) 372-5800
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1732 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1732 AA; 187874 MW; 16128552 CN;
SO

Query Match 38.3%; Score 54; DB 2; Length 1732;
Best Local Similarity 31.6%; Pred. No. 4.99e+01;
Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1097 ITAKGVSPKAIKRGRIQGT 1115
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QY 2 IDHGTGKSKVCVRQKVEGS 20

RESULT 10
ID US-08-431-333-6 STANDARD; PRT: 589 AA.
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Sequence 6, Application US/08431333
CC
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Sequence 6, Application US/08431333
CC Patent No. 5965723
CC GENERAL INFORMATION:
CC APPLICANT: Shoyad, Mohammed
CC APPLICANT: Plowman, Gregory D.
CC TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
CC TITLE OF INVENTION: MODULATING PROTEINS
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/431,333
CC FILING DATE: 27-APR-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/668,648
CC FILING DATE: 13-MAR-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mistock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 5624-161-999
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212)790-9090
CC TELEFAX: (212) 869-9741
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 589 amino acids
CC TYPE: amino acid

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CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 589 AA; 63501 MW; 1690383 CN;

Query Match      37.6%; Score 53; DB 2; Length 589;
Best Local Similarity 35.7%; Pred. No. 6.38e+01;
Matches      5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db      560 HCSARGTKLRKKI 573
QY      4 HOGTKSSKCVQKV 17
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RESULT 11
ID      PCT-US91-02321-6      STANDARD;      PRT;      589 AA.
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AC      xxxxxx
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DE      Sequence 6, Application PC/TUS9102321
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CC      Sequence 6, Application PC/TUS9102321
CC      GENERAL INFORMATION:
CC      APPLICANT: Shoyab, Mohammed
CC      APPLICANT: PLOWMAN, Gregory D.
CC      TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
CC      TITLE OF INVENTION: MODULATING PROTEINS
CC      NUMBER OF SEQUENCES: 12
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESS: 1155 Avenue of the Americas
CC      CITY: New York
CC      STATE: New York
CC      COUNTRY: USA
CC      ZIP: 10036
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/429,998
CC      FILING DATE: 27-APR-1995
CC      CLASSIFICATION: 514
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 07/668,648
CC      FILING DATE: 13-MAR-1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: MISROCK, S. Leslie
CC      REGISTRATION NUMBER: 18,872
CC      REFERENCE/DOCKET NUMBER: 5624-161-999
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (212)790-9090
CC      TELEFAX: (212) 869-9741
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 589 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 589 AA; 63501 MW; 1690383 CN;

Query Match      37.6%; Score 53; DB 2; Length 589;
Best Local Similarity 35.7%; Pred. No. 6.38e+01;
Matches      5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db      560 HCSARGTKLRKKI 573
QY      4 HOGTKSSKCVQKV 17
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RESULT 13
ID      US-07-668-648-6      STANDARD;      PRT;      589 AA.
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AC      xxxxxx
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DE      Sequence 6, Application US/07668648
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CC      Sequence 6, Application US/07668648
CC      Patent No. 5416192
CC      GENERAL INFORMATION:
CC      APPLICANT: Shoyab, Mohammed
CC      APPLICANT: PLOWMAN, Gregory D.
CC      TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
CC      TITLE OF INVENTION: MODULATING PROTEINS
CC      NUMBER OF SEQUENCES: 12
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XX      Sequence 6, Application US/08429998
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DE      Sequence 6, Application US/08429998
XX      Patent No. 5885961
CC      GENERAL INFORMATION:
CC      APPLICANT: Shoyab, Mohammed
CC      APPLICANT: PLOWMAN, Gregory D.
CC      TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
CC      TITLE OF INVENTION: MODULATING PROTEINS
CC      NUMBER OF SEQUENCES: 12
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESS: 1155 Avenue of the Americas
CC      CITY: New York
CC      STATE: New York
CC      COUNTRY: USA
CC      ZIP: 10036
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/429,998
CC      FILING DATE: 27-APR-1995
CC      CLASSIFICATION: 514
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 07/668,648
CC      FILING DATE: 13-MAR-1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: MISROCK, S. Leslie
CC      REGISTRATION NUMBER: 18,872
CC      REFERENCE/DOCKET NUMBER: 5624-161-999
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (212)790-9090
CC      TELEFAX: (212) 869-9741
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 589 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 589 AA; 63501 MW; 1690383 CN;

Query Match      37.6%; Score 53; DB 2; Length 589;
Best Local Similarity 35.7%; Pred. No. 6.38e+01;
Matches      5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db      560 HCSARGTKLRKKI 573
QY      4 HOGTKSSKCVQKV 17
      | : : : : | : | :
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RESULT 13
ID      US-07-668-648-6      STANDARD;      PRT;      589 AA.
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DE      Sequence 6, Application US/07668648
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CC      Sequence 6, Application US/07668648
CC      Patent No. 5416192
CC      GENERAL INFORMATION:
CC      APPLICANT: Shoyab, Mohammed
CC      APPLICANT: PLOWMAN, Gregory D.
CC      TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
CC      TITLE OF INVENTION: MODULATING PROTEINS
CC      NUMBER OF SEQUENCES: 12
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CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/668,648
CC FILING DATE: 19910819
CC CLASSIFICATION: 514
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mistrock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 5624-161-999
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212)790-9090
CC TELEFAX: (212) 869-9741
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 589 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 589 AA; 63501 MW; 1690383 CN;
SQ
Query Match 37.6%; Score 53; DB 1; Length 589;
Best Local Similarity 35.7%; Pred. No. 6,386+01;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
Db 560 HCSARGTKCLRRKI 573
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4 HOGTKSKCVROKV 17
QY
RESULT 14
ID PCT-US95-07754A-6 STANDARD; PRT; 652 AA.
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DE Sequence 6, Application PC/TUS9507754A
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CC Sequence 6, Application PC/TUS9507754A
CC GENERAL INFORMATION:
CC APPLICANT: Baker, Barbara J
CC APPLICANT: Whitlam, Steven A
CC TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Margaret A. Connor, USDA-ARS
CC STREET: 800 Buchanan Street
CC CITY: Albany
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94710
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/07754A
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Connor, Margaret A

CC REGISTRATION NUMBER: 30043
CC REFERENCE/DOCKET NUMBER: 0094.94
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (510) 559-6067
CC TELEFAX: (510) 559-5777
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 652 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 652 AA; 75261 MW; 2155152 CN;
SQ
Query Match 37.6%; Score 53; DB 4; Length 652;
Best Local Similarity 31.3%; Pred. No. 6,386+01;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Db 156 DNRKTDADCIROIVD 171
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RESULT 15
ID US-08-261-663A-6 STANDARD; PRT; 652 AA.
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DE Sequence 6, Application US/08261663A
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CC Sequence 6, Application US/08261663A
CC Patent No. 5571706
CC GENERAL INFORMATION:
CC APPLICANT: Baker, Barbara J
CC APPLICANT: Whitlam, Steven A
CC TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Margaret A. Connor, USDA-ARS
CC STREET: 800 Buchanan Street
CC CITY: Albany
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94710
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/261,663A
CC FILING DATE:
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Connor, Margaret A
CC REGISTRATION NUMBER: 30043
CC REFERENCE/DOCKET NUMBER: 0094.94
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (510) 559-6067
CC TELEFAX: (510) 559-5777
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 652 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 652 AA; 75261 MW; 2155152 CN;
SQ
Query Match 37.6%; Score 53; DB 1; Length 652;
Best Local Similarity 31.3%; Pred. No. 6,386+01;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 156 DNRDXTDADCIRQIVD 171
|:: : |::| |:
QY 3 DHQGTKSSKCVROKVE 18

Search completed: Wed Sep 6 08:17:55 2000
Job time : 9 secs.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 19:19:44 ; Search time 1890.83 Seconds
(without alignments)
705.070 Million cell updates/sec

Title: US-08-487-2833-8
Perfect score: 747
Sequence: 1 ARGCCGATATCCAGATGAC.....TGGTCACTGCTCGAGCTGA 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 972840 segs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBml:*
1: gb_bal:*
2: gb_bal2:*
3: gb_om:*
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5: gb_pat:*
6: gb_ph:*
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8: gb_pl2:*
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67: gb_htg18:*
68: gb_htg19:*
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78: gb_htg29:*
79: gb_htg30:*
80: gb_htg31:*
81: gb_v11:*
82: gb_v12:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	294	39.4	819	5 A18692	A18692 Synthetic n
2	283.4	37.9	723	5 AR003797	AR003797 Sequence
3	283.4	37.9	723	5 AR010133	AR010133 Sequence
4	283.4	37.9	723	5 AR055339	AR055339 Sequence
5	283.4	37.9	723	5 I11980	I11980 Sequence 92
6	283.4	37.9	723	5 I40550	I40550 Sequence 89
7	262	35.1	888	14 AF132308	AF132308 Synthetic
8	258.6	34.6	902	14 XX049832	XX049832 Synthetic s
9	250	33.5	729	5 AR027053	AR027053 Sequence
10	250	33.5	729	5 I13036	I13036 Sequence 3
11	250	33.5	729	23 E10362	E10362 cDNA encodl
12	249.2	33.4	780	14 SYN1985CF	SYN1985CF Synthetic s
13	247.2	33.1	916	5 I45604	I45604 Sequence 29
14	245.6	32.9	828	12 MM295478	MM295478 Mus musculu
15	239.6	32.1	1149	5 A63778	A63778 Sequence 42
16	239.6	32.1	1212	5 A63772	A63772 Sequence 36
17	239.6	32.1	1422	5 A63768	A63768 Sequence 32
18	239.6	32.1	1545	5 A63770	A63770 Sequence 34
19	239.6	32.1	1956	5 A63776	A63776 Sequence 38
20	239.6	32.1	2079	5 A63776	A63776 Sequence 40
21	239.4	32.0	801	14 AF021160	AF021160 Synthetic
22	236.6	31.7	733	5 AR027763	AR027763 Sequence
23	234.4	31.4	721	5 AR027762	AR027762 Sequence
24	232.8	31.2	720	5 E13599	E13599 DNA encodin

Db 121 GGGAAAGCTCTTAAGACCTGATCTATCTGCAACACATTTGGAACTGGGGTCCATCA 180
QY 187 CGCTTCTGATCCGCTCCGGAACGGATTCTACTGACATCAGCAGTCTGAGCCT 246
Db 181 AGGTTCAGTGGCATGGATCTGGGACAGATTATCTCACCATCAGACAGCTGCAATAT 240
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QY 307 GATACCAAGGAGGAAATTAACCTACTGCGGTGGTGTCTGCGGGGGTGGATCTGCT 366
Db 301 GGACACCAAGCTTGAGATGAAA-----GGTGGCGGTGATCTGGTGAAGTGGGTCGGA 354
QY 367 GTGGCGGTTCTCAAGTCCAACTGATCCGAGCCGAGGTCAAGAACCAAGGAGGCC 426
Db 355 GGTGGAGGATCTGAGATCCAGTGTGATGATCTGAGAGAGGCGCTGGTAAAGCTTGAGGG 414
QY 427 TCAGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTTATTTGATTCATGG 486
Db 415 TCCGTGAGATCTCTGCGCAGCTTCTGGTATACCTTCACAACTATGGAATGAATGG 474
QY 487 GTGGCTAGGCCCCCGGAGGCGCTGGAATGATGGGTGAGATCTTACCGGCTCTGCT 546
Db 475 GTGGCCAGGCTCCAGGAAAGGTTTAAAGTGAAGTGGGCTGGATTAACACCCACTGGA 534
QY 547 AGCAGCAATATACCGAAATTTTAAAGACCGTGTACTATGACGCTGACACTCGACT 606
Db 535 GAGCCAACTATGCTGATTTCTTCAAGGAGCGTTTACCTTCTCTTGGACATCTAAG 594
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Db 595 AACACTGCTATTTACAGATCAACAGCTCAGAGCCGAGACAGCGCTGTGATTTCTGT 654
QY 667 GCGGCTATTTTGTGTTAGCCCAATTTGATTTTGAATGTTGGGGTCAAGAAAC 726
Db 655 ACAAGACGGGGTTACG-----ACTGTACTTCGATGCTGGGGCCCAAGGAGACC 702
QY 727 CTGTCACTGTCTGAGCTGA 747
Db 703 ACGGTACCGTCTCTCATGA 723

RESULT 3
LOCUS AR010133 723 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 89 from patent US 5756699.
ACCESSION AR010133
VERSION AR010133.1 GI:3968938
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 723)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5756699-A 89 26-May-1998;
FEATURES
source 1..723
BASE COUNT 178 a 162 c 207 g 176 t
ORIGIN

Query Match 37.9%; Score 283.4; DB 5; Length 723;
Best Local Similarity 63.7%; Pred. No. 5.3e-71;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

QY 67 ATCACTGCGGCGCCAGCCAAACATCTATGCGCGCTGAACCTGATTAACGTAACT 126
Db 61 ATCACTGCGGCGGCGAGCTAGGACATTAATACCTATTTAAAGTGTTCAGAGAAACCA 120
QY 127 GGGAAAGCTCCGAGCTTCTGATTTACGTTGGAGAAACCTGGCAGATGAGATCCCTTCT 186
Db 121 GGGAAAGCTCTTAAGACCTGATCTATCTGCAACACATTTGGAACTGGGGTCCATCA 180
QY 187 CGCTTCTGATCCGCTCCGGAACGGATTCTACTGACATCAGCAGTCTGAGCCT 246
Db 181 AGGTTCAGTGGAGTGGATCTGGGACAGATTATCTCACCATCAGACAGCTGCAATAT 240
QY 247 GAAGACTTTCCTACGATTTACTGTGACAGCTTTTAAATACTCCGTGACTTTCGACAG 306
Db 241 GAAGATTTTGAATTTATTTATTTCAACAGATGATGAGTCTCCGTGACGTTCCGTGA 300
QY 307 GGTACCAAGCTGGAATTAACCTACTGCGGTGGTGTCTGCGGGCGGTGAGATCTGCT 366
Db 301 GGACACCAAGCTTGAGATGAAA-----GGTGGCGGTGATCTGGTGAAGTGGGTCGGA 354
QY 367 GTGGCGGTTCTCAAGTCCAACTGATCCGAGCCGAGGTCAAGAACCAAGGAGGCC 426
Db 355 GGTGGAGGATCTGAGATCCAGTGTGATGATCTGAGAGAGGCGCTGGTAAAGCTTGAGGG 414
QY 427 TCAGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTTATTTGATTCATGG 486
Db 415 TCCGTGAGATCTCTGCGCAGCTTCTGGGATACCTTCACAACTATGGAATGAATGG 474
QY 487 GTGGCTAGGCCCCCGGAGGCGCTGGAATGATGGGTGAGATCTTACCGGCTCTGCT 546
Db 475 GTGGCCAGGCTCCAGGAAAGGTTTAAAGTGAAGTGGGCTGGATTAACACCCACTGGA 534
QY 547 AGCAGCAATATACCGAAATTTTAAAGACCGTGTACTATGACGCGGTGACACTCGACT 606
Db 535 GAGCCAACTATGCTGATTTCTTCAAGGAGCGTTTACCTTCTCTTGGACATCTAAG 594
QY 607 AGTACAGTATACATGAGCTCTCCAGCTGCGATCGAGAGACAGCGCCCTATATTATTC 666
Db 595 AACACTGCTATTTACAGATCAACAGCTCAGAGCCGAGACAGCGCTGTGATTTCTGT 654
QY 667 GCGGCTATTTTGTGTTAGCCCAATTTGATTTTGAATGTTGGGGTCAAGAAAC 726
Db 655 ACAAGACGGGGTTACG-----ACTGTACTTCGATGCTGGGGCCCAAGGAGACC 702
QY 727 CTGTCACTGTCTGAGCTGA 747
Db 703 ACGGTACCGTCTCTCATGA 723

RESULT 4
LOCUS AR055339 723 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 89 from patent US 5837491.
ACCESSION AR055339
VERSION AR055339.1 GI:5980916
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 723)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Polynucleotides encoding gelonin sequences
JOURNAL Patent: US 5837491-A 89 17-NOV-1998;
FEATURES
source 1..723
BASE COUNT 178 a 162 c 207 g 176 t
ORIGIN

Query Match 37.9%; Score 283.4; DB 5; Length 723;
Best Local Similarity 63.7%; Pred. No. 5.3e-71;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

ORIGIN

Query Match 37, 98; Score 283.4; DB 5; Length 723;
Best Local Similarity 63.7%; Pred. No. 5.3e-71;
Matches 472; Conservative 0; Mismatches 25; Indels 18; Gaps 2;

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Db 1 GACATCCAGATGACTCAGTCTCCATCTCCCTGTCTGCTGTAGGAGACAGAGTCACT 60

QY 67 ATCACTGGCGGCGACGAGAAACATCTATGGCGGCTGAACTGGTATCAACGTAACCT 126
Db 61 ATCACTGGCGGCGAGTCAAGACATTAATAGCTATTTAAGCTGTTTCCAGCAGAAACCA 120

QY 127 GGAAGAGTCCGAGCTCTGATTTACGTTCCGAGCAGACCTGGCAGATGGAGTCCCTTCT 186
Db 121 GGAAGAGTCTTAAGACCTCTGATCTATCTGCAACAGATTGGGATCTGGGTCCTATCA 180

QY 187 CGTTTCTCTGGATCCGCTCCGAAACGATTTCACTCTGACCATCAGAGTCTCGAGCT 246
Db 181 AGTTTCACTGGCAGTGGATCTGGGACAGATTAATCTCTCACCATCAGAGCTGCAATAT 240

QY 247 GAAGACTTCGCTACGATTAATCTGTCAGAACTTTTAAATCTCCGTTGACATTCGGACAG 306
Db 241 GAAGATTTTGGAAATTTATTTATTTGTCACAGATGATGAGTCTCCGTCGACCTTCGGTGA 300

QY 307 GGTACCAAGTGGAAATAAACGTTACTGGCGGTGTTCTGTGGCGGTGGATCTGGT 366
Db 301 GGCACCAAGCTTGAGATGAAA-----GGTGGCGGTGGATCTGGTGGAGTGGGTCCGGA 354

QY 367 GGTGGCGGTCTCAAGTCCAACTGGTGCATCCGCGCGGAGGTCAAGAACCCAGGGGCC 426
Db 355 GGTGGAGATCTGAGATCCAGTCTGGAGGAGGCTGGTGAACCTGGAGGG 414

QY 427 TCAGTCAAGTGTCTGTAAGCTAGCGGTATATTTTCTTAATTTATTTGATTTCAATGG 486
Db 415 TCCGTGAGATCTCTCGCAGCTTCTGGGTATACCTTTCACAACTATGGAATGAATGG 474

QY 487 GTGGTCAAGCTCCGCGAGGCTGGAATGGATGGTGGATGAGTCTTACCGGGCTCTGGT 546
Db 475 GTGGCGAGCTCCAGAAAGGTTTATAGTGGATGGGCTGGATTAACCCACACTGGA 534

QY 547 AGCACCAATATACGAAATTTTAAAGACCGTGTACTATGACGCTGACACTTCGACT 606
Db 535 GAGCCACATATGCTGATCTTCAAGGAGCGTTTACCTCTCTTTGGAGATCTTAAG 594

QY 607 AGTACATATACATGAGCTCTCCAGCCTCGCATCGGAGACACGCGCTCTATTATTGC 666
Db 595 AACACTGCCCTATTACAGATCAACAGCTCAGAGCGGAGGACACGCTGTGTATTCTGT 654

QY 667 GCGGTTATTTTGGTCTAGCCGAAATTTGATTTTGGTGGTGGTGGTGGTGGTGGTGGT 726
Db 655 ACAAGACGGGTTACG-----ACTGGTACTTCGATGTCTGGGCGCAAGGGACC 702

QY 727 CTGGTCACTGTCTCGAGCTGA 747
Db 703 ACGGTACCGTCTCTCTCATGA 723

RESULT 5
LOCUS I11980 723 bp DNA PAT 26-JUL-1995
DEFINITION Sequence 92 from Patent US 5416202.
ACCESSION I11980
VERSION I11980.1 GI:909423
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 723)
AUTHORS Bernhard, S.L., Better, M.D., Carroll, S.F., Lane, J.A. and Lei, S.
TITLE Materials comprising and methods of preparation and use for ribosome-inactivating proteins
JOURNAL Patent: US 5416202-A 92 16-MAY-1995;
FEATURES Location/Qualifiers
1..723 /organism="unknown"
BASE COUNT 178 a 162 c 207 g 176 t

QY 7 GATATCCAGATGACCCAGTCCCGTCTCCCTGTCCGCTCTGTGGCGATGAGGTCAACC 66
Db 1 GACATCCAGATGACTCAGTCTCCATCTCCCTGTCTGCTGTAGGAGACAGAGTCACT 60

QY 67 ATCACTGGCGGCGACGAGAAACATCTATGGCGGCTGAACTGGTATCAACGTAACCT 126
Db 61 ATCACTGGCGGCGAGTCAAGACATTAATAGCTATTTAAGCTGTTTCCAGCAGAAACCA 120

QY 127 GGAAGAGTCCGAGCTCTGATTTACGTTCCGAGCAGACCTGGCAGATGGAGTCCCTTCT 186
Db 121 GGAAGAGTCTTAAGACCTCTGATCTATCTGCAACAGATTGGGATCTGGGTCCTATCA 180

QY 187 CGTTTCTCTGGATCCGCTCCGAAACGATTTCACTCTGACCATCAGAGTCTCGAGCT 246
Db 181 AGTTTCACTGGCAGTGGATCTGGGACAGATTAATCTCTCACCATCAGAGCTGCAATAT 240

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Db 241 GAAGATTTTGGAAATTTATTTATTTGTCACAGATGATGAGTCTCCGTCGACCTTCGGTGA 300

QY 307 GGTACCAAGTGGAAATAAACGTTACTGGCGGTGTTCTGTGGCGGTGGATCTGGT 366
Db 301 GGCACCAAGCTTGAGATGAAA-----GGTGGCGGTGGATCTGGTGGAGTGGGTCCGGA 354

QY 367 GGTGGCGGTCTCAAGTCCAACTGGTGCATCCGCGCGGAGGTCAAGAACCCAGGGGCC 426
Db 355 GGTGGAGATCTGAGATCCAGTCTGGAGGAGGCTGGTGAACCTGGAGGG 414

QY 427 TCAGTCAAGTGTCTGTAAGCTAGCGGTATATTTTCTTAATTTATTTGATTTCAATGG 486
Db 415 TCCGTGAGATCTCTCGCAGCTTCTGGGTATACCTTTCACAACTATGGAATGAATGG 474

QY 487 GTGGTCAAGCTCCGCGAGGCTGGAATGGATGGTGGATGAGTCTTACCGGGCTCTGGT 546
Db 475 GTGGCGAGCTCCAGAAAGGTTTATAGTGGATGGGCTGGATTAACCCACACTGGA 534

QY 547 AGCACCAATATACGAAATTTTAAAGACCGTGTACTATGACGCTGACACTTCGACT 606
Db 535 GAGCCACATATGCTGATCTTCAAGGAGCGTTTACCTCTCTTTGGAGATCTTAAG 594

QY 607 AGTACATATACATGAGCTCTCCAGCCTCGCATCGGAGACACGCGCTCTATTATTGC 666
Db 595 AACACTGCCCTATTACAGATCAACAGCTCAGAGCGGAGGACACGCTGTGTATTCTGT 654

QY 667 GCGGTTATTTTGGTCTAGCCGAAATTTGATTTTGGTGGTGGTGGTGGTGGTGGTGGT 726
Db 655 ACAAGACGGGTTACG-----ACTGGTACTTCGATGTCTGGGCGCAAGGGACC 702

QY 727 CTGGTCACTGTCTCGAGCTGA 747
Db 703 ACGGTACCGTCTCTCTCATGA 723

RESULT 6
LOCUS I40550 723 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 89 from patent US 5621083.
ACCESSION I40550
VERSION I40550.1 GI:2082842
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 723)
AUTHORS Better, M.D., Carroll, S.F. and Studnicka, G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins

ACCESSION	AR027053
VERSION	AR027053.1
KEYWORDS	GI:5937893
SOURCE	.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 729)
TITLE	Shimamura,T., Hamuro,J., Nakazawa,H., Kanayama,Y., Suganuma,K. and Takeshita,T. .gamma.-chain humaninterleukin-2 receptor polypeptide and method of making
JOURNAL FEATURES	Patent: US 5856140-A 3 05-JAN-1999; Location/Qualifiers 1..729
BASE COUNT	/organism="unknown"
ORIGIN	Source 199 a 169 c 182 g 179 t
Query Match	33.5%; Score 250; DB 5; Length 729;
Best Local Similarity	60.9%; Pred. No. 2.3e-61;
Matches 447; Conservative	0; Mismatches 275; Indels 12; Gaps 2;
Oy	7 GATATCCAGATTATGCCAGTCCCCGCTCCTCCGTCCGCTCGTGCGCATAGGGTCACC 66
Dd	4 GATATTCGCTGACACAGCTCCACGCTCCCATCTGCATCTGTGGGAACCACTGTACAC 63
Oy	67 ATCACCTCGGGCGCCGACGGAACAACATCTATGCGCGCTAACCTGGATCAAGTAACCT 126
Dd	64 ATACATATGTCGAGCAAGTGGGAATTTTACATTTATTTAGCATGGATACGAGAACAG 123
Oy	127 GGGAAAGCTCCGAGACTTCTGTATTTACGGTGGCAGCAACCTGGCAGANTGACTCCCTTCT 186
Dd	124 GGAAATATCTCCACACTCCTGCTGTATAATGCAAAAACCTTAGCAGATGGTGGCATCA 183
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Dd	184 AGGTTTCAGGGGAGTGGATCAGGAACACATTTCTTCAMAGATCAACGCTCGAGCT 243
Oy	247 GAAGACTTCGCTACGATATTTACTGTGAGAACGTATTAATATCTCCGTGACTTTCGAGAC 306
Dd	244 CAAGATTTTGGAGATTAATTAATCTGATCAACATTTTGGAGTACTCCGTGGACGTTCCGTGA 303
Oy	307 GGTACCAAGTGGAAATAAACAACGTACTGGCGGTGGTCTTGAGGCGGTGGATCTGAT 366
Dd	304 GGGACCAAGCTGGAAGCTCAA-----GTGAGAAATCCTCAGAGATCTGGCTCCGA 354
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Dd	355 TCCAAACACACCAAGTCAAACTCGAGGAGTCTGACCTGAGACTGGTGAAGCCTGGGGCT 414
Oy	427 TCAGTCAAGTGTCTGTAAAGTTCAGCGGCTATTTTTTCTAATTAATGATTCGAATG 486
Dd	415 TCAGTGAAGATATCTCTGCAAGGCTTCTGTGTTACTATTCACGTGGCTACTACATGACATGG 474
Oy	487 GTGCGTCAGGCCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCCGGCTCTGGT 546
Dd	475 GTGAAGCAAGGCATGTAAAGAGCCTTGAGTGGATTTGACGATTAATCCTTACAATGT 534
Oy	547 AGCACCGAATATACGAAAAATTTTAAAGACGCTGTACTAGTACGCGTGACACTTCGACT 606
Dd	535 GCTACTACTACAAACCAAAATTTCAAGGACAAAGCCAGCTGACTGATGATTAAGTCCTCC 594
Oy	607 AGTACAGTATACATGGAGACTCTCCAGGCTTCGCATGGGAGAGACAGCGCGCTCATATTGCG 666
Dd	595 AGCAAGGCTATACATGAGACTCCACAGCCTGCATCTGTAGGACTCTGCAGTCTATTACTGT 654
Oy	667 GCGCCTATATTTTGTCTTGCCCGAATTGGTATTTTGGATGTTTGGGTCAGAAGCA 726
Dd	655 GCAGAGAGAAATTTACTAGCGGTAGTACGAG---TTTGCTTACTGGGGCCAAAGGACT 711
Oy	727 CTGCTCACTGCTTC 740

DB	712	CTGGTCACTGCTC	725
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DEFINITION	Sequence 3 from patent US 5582826.		PAT
ACCESSION	131036		06-FEB-1997
VERSION	131036.1	GI:1821827	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 729) Shimamura,T., Hamuro,J., Nakazawa,H., Kanayama,Y., Sugamura,K. and Takeshita,T.		
TITLE	Monoclonal antibodies which bind the gamma chain of human interleukin-2 receptor		
JOURNAL	Patent: US 5582826-A 3 10-DEC-1996;		
FEATURES	Location/Qualifiers 1..729		
source	/organism="unknown"		
BASE COUNT	199 a 169 c 182 g 179 t		
ORIGIN			
Query Match	33.5%; Score 250; DB 5; Length 729;		
Best Local Similarity	60.9%; Pred. No. 2,3e-61;		
Matches	447; Conservative 0; Mismatches 275; Indels 12; Gaps 2		
DB	7	GATATTCAGATGATACCCAGTCCCGTCCCTGTCGCGCTGTGGCGATAGGTACACC	66
DB	4	GATATTCCTCTGACACAGCTCCAGCTCCCTCATCTGCACTGTGGGAAACTGTACAC	63
DB	67	ATCACCCTGGGGGGCCGACCCAAACATCTATGGGGCCCTGAACTGATCACTAACT	126
DB	64	ATCCATATGTCGAGCAAGTGGGAATATTCACAAATATTTAGCATGTGATGCGAGAAACAG	123
DB	127	GGGAAAGCTCCCAAGCTTCTGATTTACGGTGGCGACCAACCTGGCAGATGAGTCCCTTC	186
DB	124	GGAAATCTCCCTCAGCTCCTGTGCTATATGCAAAACCTTACGATGCTGTGCGATCA	183
DB	187	CGCTTCTGTGATCCGGCTCCGAGACGATTTCACTCTGCATCAGCAGCACTGCGACCT	246
DB	184	AGCTTCAGTGGCAGTGGATCAGAGAACACAAATATTTCTCTCAAGATCAACAGCTGACGCT	243
DB	247	GAAAGCTTGGCTACGATATCTGTGCAAGACGTTTAAATCTCCGTGACTTTCGACAG	306
DB	244	GAAATTTTGGGAGTATTTACTGTCAACATTTTGGAGTACTCCGTGGACGTTCCGTGG	303
DB	307	GGTACCAAGTGGGAATTAACGTACTGGCGGGTGGTCTGTGGCGGTGGATCTGGT	366
DB	304	GGGACCAAGCTGAGCTCAA-----GTGAGAAATCTTCAGAGATGTGCTCCGAA	354
DB	367	GGTGGCGGTTCTCAAGTCCCACTGTGATCCGCGCCGAGGTCAAGACCCAGGGGCC	426
DB	355	TCCAAAGACGACGAGTCAAACTCGAGGAGTGTGACCTGAGACCTGGGAAAGCCTGGGGGT	414
DB	427	TCAAGTCAAGTGTCTCTGTAAAGCTAGCGGCTATATTTTCTAATTTATGGATCAATG	486
DB	415	TCAAGTCAAGTATCTGTGCAAGGCTTGTGTTACTTCATTCAGTCTGCTACATGCACTG	474
DB	487	GTGGCGTACGGCCCCGGGGGAGGGCCGTGGAATGGATGGGTGAGATCTTAACGGGCTGTGG	546
DB	475	GTGAAGCAAAAGCATGTAAAGAGCCTTGGAGTGGATTTGAGCGTATTAATCTTCAATGGT	534
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QY 667 GCAGGTTATTTTGGTCTAGCCGAATGGTATTTTGATTTGGGTCAAGGAACC 726
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Db 712 CTGCTCACTGCTC 725

RESULT 11
E10362 ID E10362 standard; RNA; ROD; 729 BP.
XX AC E10362;
XX SV E10362.1
XX DT 08-OCT-1997 (Rel. 52, Created)
DT 08-OCT-1997 (Rel. 52, Last updated, Version 1)
XX CDNA encoding an monoclonal antibody against human Interleukin-2
DE receptor gamma chain.
XX JP 1995313188-A/2.
XX Mus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Teleostomi;
OC Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
OC Mus.
XX [1]
RN 1-729
RP Shimamura T., Hamuro J., Nakazawa H., Kanayama Y., Sugamura K.,
RA Takeshita T.;
RT "IMMUNOSUPPRESSIVE AGENT";
RL Patent number JP 1995313188-A/2, 05-DEC-1995.
RL AJINOMOTO CO INC, SUGAMURA KAZUO..
XX OS Mus sp. (mouse)
CC PN JP 1995313188-A/2
CC PD 05-DEC-1995
CC PF 21-APR-1993 JP 93P 94491, 07-MAR-1994 JP 94P 36065
CC PR 21-APR-1993 JP 93P 94491, 07-MAR-1994 JP 94P 36065
CC PI SHIMAMURA TOSHIAKI, HAMURO JUNJI, NAKAZAWA HARUMI,
CC PI KANAYAMA YUKA,
CC PI SUGAMURA KAZUO, TAKESHITA TOSHIICHI
CC PC C12P21/08.A61K39/395.A61K39/395.C12N1/21.C12N5/20,
CC PC C12N15/13//C12N15/06,
CC PC (C12P21/08.C12R1:19).(C12P21/08.C12R1:91).(C12N1/21.C12R1:19);
CC FH Key Location/Qualifiers
CC FT source 1..729
CC FT /organism="Mus sp."
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CC FT mat_peptide 1..729
CC FT /product="anti-IL-2 receptor gamma chain"
XX XX Location/Qualifiers
FH FT source 1..729
FH FT /db_xref="taxon:10095"
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XX SQ Sequence 729 BP; 199 A; 169 C; 182 G; 179 T; 0 other;

Query Match 33.5%; Score 250; DB 23; Length 729;
Best Local Similarity 60.9%; Pred. NO. 2.3e-61;
Matches 447; Conservative 0; Mismatches 275; Indels 12; Gaps 2;
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Db 4 GATATTCGTGACACAGTCTCCAGCCTCCCTATCGCATCTGTGGGAGAAACTGTCCACC 63
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LOCUS Synthetic single chain Fv (N19-8 scFv) DNA fragment.
DEFINITION L43067
ACCESSION L43067.1 GI:870721
VERSION complement C5 inhibitor; inclusion body protein.
KEYWORDS Synthetic construct DNA.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 780)
AUTHORS Evans, M.J., Rollins, S.A., Wolff, D.A., Rother, R.P., Norin, A.J.,
Th, D.M., Mueller, J.P., Nye, S.H., Squinto, S.P., and Wilkins, J.A.
TITLE In vitro and in vivo inhibition of complement activity by a
single-chain Fv fragment recognizing human C5
JOURNAL Mol. Immunol. (1995) In press
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BASE COUNT
ORIGIN

188 a 195 c 216 g 181 t

Query Match	33.4%	Score 249.2	DB 14	Length 780
Best Local Similarity	59.4%	Pred. No. 3.9e-61		
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OY	1	ATGGCGGATATACAGATGACCCAGTCCCGCTCCCTCCGCGCTGTGGGCGATAGG	60	
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OY	61	GTACCATTCACCTCGGGGCGCCAGCGAAAAACAT-----CTATGGCGCGGTGAC	108	
Db	61	GCCACCATATCTCTGCAGAGACCAGTGAAAGTGTGATAGTTATGACATATGTTTATGCAC	120	
OY	109	TGGTATCAACGTAAACCTTGGGAAAGCTCCGAAGCTTCTGATTTAGCGTGCAGAACCTG	168	
Db	121	TGGTACCGACGAATAACAGAGACAGCCACCCAACTCTCATCTTTCTTGTCATCACTCA	180	
OY	169	GCAGATGGAGTCCCTTCTGCTTCTCTGTGATCCGGCTCCGAAAGGATTTCACTGTACC	228	
Db	181	GAATCTGGGGTCCCTGCCAGTTCATGATGAGCAGTGGGTCTAGGACAGACTTCAACCTCACC	240	
OY	229	ATCAGACGCTCTCAGCCCTGTAAGACTTCCTGCTACGTATTTACTGTGACAGCTTTAAATACT	288	
Db	241	ATTGATCTCTGTGGAGGCTGATGATCATCTGCAACCTATTTACTGTACAGAAATATAGAGTT	300	
OY	289	CCGTTGACTTTGGGACAGGGGTACCAAGGTGGAAATATAACGTAACCTGCGCGTGGTCTT	348	
Db	301	CCGAACAGCTTGGGAGGGGGGACCAAGCTGGAAATATAAACGGAGCGGAGTGGCGGTG	360	
OY	349	GGTGGCGGTGATCTGATGTTGGTGGCGTTCCTCAAGTCCCACTGGTGCATCCGCGCCGAG	408	
Db	361	GGTGGCGGGGAGTCCGGGTGGCGGAGGGTGGAGCTGACAGTCAAGCTGTGTGAGTCTTGGGAGAC	420	
OY	409	GTCAAGAAGCCAGGGGCGCTCAGTCAAAAGTGTCTGTAAAGCTAGCGGCTATATTTTTCT	468	
Db	421	TTAGTAGAGCTTGGAGGGGTCCCTGAACATCTCTGTGACAGCTCTGGAATTCACCTTAGT	480	
OY	469	AATTTATGGATTCAATGGGTGCTGACAGGCCCGCGGAGCGCTTGGAATGATGGGTGAG	528	
Db	481	AGCTATTATATCTTGTGGTGTGCGCAGATTTTCAGAGAAGAGCGCTGAGTGTGTCGACGC	540	
OY	529	ATCTTACCGGGCTCTGTGTAGCACCCGATATACCGAAATTTTAAAGACCGGTTTACTATG	588	
Db	541	ATTAAATAGTAATGTGTATGACACTACTACTACAGACAGTGTAAAGGCGCGATTCACCATC	600	
OY	589	ACGGGTGACACTTCGACTGTACAGTATTCATAGSAGCTCTCCAGCTGTGATCGGAGGC	648	
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OY	649	ACGGCGGCTATTTATTTGCGCGGCTATTTTATTTTGTGTTACGCGCAATTGGATTTTGTAT	708	
Db	661	ACAGCTTGATATTTCTGTGTATAGAGAGACTTATTTACTACGGGATTAATGCCCTTTCGAT	720	
OY	709	GTTTGGGGTCAAGAACCTGTGTACTGTCTC	740	

Db	721	GTCTGGGGCAGGACGACGCTACCGTCTC	752
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LOCUS	145604		
DEFINITION	145604	916 bp	DNA
ACCESSION	145604		PAT
VERSION	145604.1	GI:2469706	07-OCT-1997
KEYWORDS			
SOURCE	Unknown:		
ORGANISM	Unknown:		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 916)		
	Lebetter,J.A., Gilliland,L.K., Hayden,M.S., Linsley,P.S.,		
	Bajorath,J. and Fell,H.Perry.		
	Expression vectors encoding bispecific fusion proteins and methods		
	of producing biologically active bispecific fusion proteins in a		
	mammalian cell		
	Patent: US 5637481-A 29 10-JUN-1997;		
JOURNAL			
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BASE COUNT	254 a 223 c 228 g	211 t	
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	Best Local Similarity	60.2%	Pred. No. 1.5e-60;			
	Matches 449;	Conservative	0; Mismatches 288;	Indels	9;	Gaps 2;
QY	4	GGCGATTCACATCAATACCAGTCCCGCTCCTCCCTGTCGCCCTGTGGGCATAGGCTC	63			
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Dd	133	ACCATCAGTTGGAGGGCCAAGTCAGGCATCTCCAAATTATTAACTGTATCAGCAGAAA	192			
QY	124	CCTGGAAAAAGCCCCGAAGTCTGTGATTTTCGCGTGCGACACAACCTGGCAATGAGNCCCT	183			
Dd	193	CCAGATGGAAGCTGTTAAACTCCTGATCTACTACATCAAGATTACATCAGAGATCCCA	252			
QY	184	TCTCGCTTCTCTGATCCGGCTCCGGAAAGGATTTCACTGACCATCAAGCTGCGAG	243			
Dd	253	TCAAAGTTTCAGTGGCAGTAGTGGGTCTGGAAACAGAATTATTTCTCACCATTCGCCAACCTGC	312			
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Dd	313	CCAGAAGATATTGCCACTACTTCTTGGCCAAAGGGTAATAACCTTCCGTGGACGTTCCGT	372			
QY	304	CAGGCTACCAAGGTGGAAATAAAGC---TACTGGCGGTGTGGTCTCTGTGGCGGTGA	360			
Dd	373	GGAGGCACCAAACTGTATACCAAAAGGGAGGTCGGTGGCGGTGGCTCGGGCGGTGTGG	432			
QY	361	TCTGTGTGTGGCGGTTCTC-----AAGTCCAACTGTGTCAATCCGGCCCCAGGTCAAG	414			
Dd	433	TGGGTGTGGGGGGGATCTATCGATGAGGTGCTGACCTGCAACAGCTGTGGACTGAGCTGAGT	492			
QY	415	AAGCCAGGGGCTCATGTCAAAGTGTCCGTTAAAGCTAGAGGGCTATATTTTTCTAATT	474			
Dd	493	AAGCTGTGAGCTTCATATGACATGTCTCTCCAAAGGCTCTGTGTACTCATTTCACTGGCTAC	552			
QY	475	TGGATTCAATGGGTGCGTCAGGCCCCCAGGGCAGGGCCTGGAATGATGGGTGAGATCTTA	534			
Dd	553	ATCGTAAGTGTGCTGAGACAGAGCCATGAAAGAACTTGAGTGGATTTGACTTATTAAT	612			
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Dd	613	CCATCAAAAGGCTTCTACTACTTACCAACCGAAATTTCAAGGGCAAGGCCCATTTACTGA	672			
QY	595	GACACTTGACTAGTACAGTATATACAGTCTCCAGCTCGATCGAGAGACAGGCC	654			

Query Match 32.1%; Score 239.6; DB 5; Length 1149;
Best Local Similarity 62.0%; Pred. NO. 2.3e-58;

	Matches	439;	Conservative	0;	Mismatches	224;	Indels	45;	Gaps	27
OY	6	CGATATCCAGATGACCCAGTCCCGCTCCTCCCTGTCGCCCTCTGTGGCGGATAGGGTCA	65							
Db	60	CGATATCCAGATGACGATCAGATGTCACAAATGACTACTGTCAGTGCCTAGGTAGGTAGGGGTCA	119							
OY	66	CATCACCTGGCGGCGCAGGAAACATCT	110							
Db	120	CATCACCTGTGAGAGTAGTAAAGTCTCTCCATAGTAAAGGTGACACCTTCTCTATTG	179							
OY	111	GTATTAACGTAACCTGGGAAAGCTCCGAAAGCTTGTATTACGGGTGCACCAACCTG	170							
Db	180	GTTCCAGCAGAAACACAGGTAAGAGCCCAAGCTCCTCATGTTAGATGATAGTAACTGCC	239							
OY	171	AGATGAGTCCCTCTCCGCTCTCTGATCGGGCTCCGGACGGATTTCTACTGACCAT	230							
Db	240	CAGTGGTACCATCTAGTTCAGTGTAGTGGTATGGTATGATGATTCACCTCTCAT	299							
OY	231	CAGCAGTCTGCAGCCTGAAGACTTGGCTACGATATACGTTCAGAACGTTTAAATATCTC	290							
Db	300	CAGATGCTCCACGCGAGATGATTTGCCACTTATTATGTATGACAGCATCTCGAATATCC	359							
OY	291	GTTGACTTCCGACAGGGTACCAAGTGGAAATTAACCTACTGACGG	338							
Db	360	ATTCACTTTCGGTCAAGGACTACTAAGTAGAATATAAACGTACGGGTGGCGGAGGCTCAG	419							
OY	339	-----TGGTGTCTTGCTGGTGGCGGCGGTGATCTGGTGTGGCGGTTCTCA	380							
Db	420	TGGCGAGAGGTCAGGTGGCGGAGGGTCAAGGTGGCGAGGGTCAAGTGGCGGAGGGTCA	479							
OY	381	AGTCAACTGTGTGCAATCCGGCGCGAGGTCAAGAACCGAGGGCCTCAGTCAAAAGTGC	440							
Db	480	GATTGAGTGTGTGACGTGTGGAGCAGAGGTGAAGAACCTGGATTTCTGTAAAGGTGTC	539							
OY	441	CTGTAAACCTAGCGGCTATATTTTCTATATATGATTCATAGGGTGCCTCAGGCCCC	500							
Db	540	TTGTAAAGCATCTGATATACCTTACCGGACTACTACATTAATTTGATGATGACAGGCAAC	599							
OY	501	CGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATAC	560							
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Db	660	TGAGAAAGTTCAGAGGAAAGCAACACTGACATGACACATCCAGAAATACCGCTACAT	719							
OY	621	GGAGCTTCCAGCGCTGCAGTCGAGAGACACGGCGCTTATTTTTCGCG	668							
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 19:06:43 ; Search time 930.19 seconds
(without alignments)
3541.364 Million cell updates/sec

Title: US-08-487-283a-8
Perfect score: 747
Sequence: 1 ATGCCGATATCCAGATGAC.....TGGTCACTGCTCGAGCTGA 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues 10495684
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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RESULT 4
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ACCESSION AW406294
VERSION AW406294.1 GI:6925351
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 471)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On May 11, 1999 this sequence version replaced gi:4776604.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
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                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 115 a 132 c 110 g 114 t
ORIGIN

Query Match 24.7%; Score 184.6; DB 72; Length 471;
Best Local Similarity 71.1%; Pred. No. 1.7e-46;
Matches 244; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 7 GATATCCAGATGACCCAGTCCCGCTCCCTCCCTGTGGCGGTAGAGGTCAACC 66
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Db 117 ATCACTTCGGCGACAGTACACAGCATTAGAACCTATTTAAATGGTATCAGCAGAAACCA 176

QY 127 GGGAAAGCTCCGAAGCTTCTGATTACGGTGCAGCAACCTGGCAGATGAGTCCCTTCT 186
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Db 177 GGGAAAGCCCTTAACCTCTGTATCTATGCTGATCCTGATCAGTTTGAAGTGGGTCCCATCA 236

QY 187 CGCTTCTCTGGATCCGGTCCCGAAGCGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246
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Db 237 AGGTTCAAGTGGCAGTGGAFTCTGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCT 296
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Db 297 GAAGATTTTGGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGAGCTCGGCCCA 356
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QY 307 GGTACCAAGTGGAAATAAAAGCTACTGGCGTGTGGTGTCTTG 349
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Db 357 GGGACCAAGGTGGAAGTCAACAGCACTGTGGCTGCACCATCTG 399

RESULT 5
AW406081 566 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BLO-aco-b-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3060700 5', mRNA sequence.
ACCESSION AW406081
VERSION AW406081.1 GI:6925102
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 566)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On May 11, 1999 this sequence version replaced gi:4776388.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
FEATURES
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                /cell_line="MGC85"
                /lab_host="DH10B (LTI)"
                /note="Vector: p7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 138 a 157 c 143 g 128 t
ORIGIN

Query Match 24.7%; Score 184.6; DB 72; Length 566;
Best Local Similarity 71.1%; Pred. No. 1.8e-46;
Matches 244; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 7 GATATCCAGATGACCCAGTCCCGCTCCCTCCCTGTGGCGGTAGAGGTCAACC 66
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Db 65 GACATCCAGATGACCCAGTCTCCATCTCCCTGTGCGCATCTGTAGGACAGAGTCAACC 124

QY 67 ATCACTTCGGCGCCAGGAAACATCTATGGCGCGCTGAACCTGGTATCAAGTAAACCT 126
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QY 127 GGGAAAGCTCCGAAGCTTCTGATTACGGTGCAGCAACCTGGCAGATGAGTCCCTTCT 186
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Db	185	GGGAAAGCCCTTACGCTCCTGATCTATGATGTCATCCATCTTGCAGAGGTGGGTCCCATCC	244
Qy	187	CGCTTCTCTGATCCGGGCTCCGGAACGGATTTCACCTCTGACCATCAGAGTGTGCAGCCT	246
Db	245	AGATTCACTGAGTGGATCTGTGGAGACAGATTTCACCTCTCCACCGTCAGGCTGTGGAACCT	304
Qy	247	GAGACCTTCGCTACGATATCTGTCAGAAAGCTTTTAATACATCCGTTGACTTTCGGACAG	306
Db	305	GAGGATTTTGGCAGCTTACTACTGTCTACACAGATTTACACTACCCCGCTCACTTTCGGCGGA	364
Qy	307	GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGTGTCTCG	349
Db	365	GGGACCAAGGTGGAAATCAAAAGCACTGTGGTGCACCATCTG	407
RESULT	6		
LOCUS	AM404714	608 bp	EST
DEFINITION	UI-HF-BL0-acc-c-11-0-ur.r1 NIH_MGC_37	Homo sapiens	cDNA clone
ACCESSION	AM404714		
VERSION	AM404714.1	GI:6923771	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 608)		
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	On Jan 6, 2000 this sequence version replaced gi:6673638.		
	Contact: Robert Strausberg, Ph.D.		
	Tel.: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	Eco RI site shown at the beginning of the sequence.		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
	cDNA Library Preparation: M.B. Soares Lab		
	cDNA Library Arrayed by: M.B. Soares Lab		
	DNA Sequencing by: M.B. Soares Lab		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/MLML at: www-bio.llnl.gov/dbp/imag/image.html		
	Seq primer: M13 Forward.		
FEATURES	Location/Qualifiers		
source	1..608		
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	/clone_lib="NIH_MGC_37"		
	/tissue_type="lymph"		
	/cell_type="germinal center B cells"		
	/cell_line="MGC85"		
	/lab_host="DH10B (LT1)"		
	/note="vector: pT773-Pac; Site.1: NotI; Site.2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
BASE COUNT	158 a 169 c 146 g 135 t		
ORIGIN			
Query Match	24.5%;	Score 183.2;	DB 72; Length 608;
Best Local Similarity	71.2%;	Pred. No. 5e-46;	
Matches 242;	Conservative 0;	Mismatches 98;	Indels 0; Gaps 0;
Qy	10	ATCCAGATGACCGACGATCCCGCTCCTCTGTCGGCTCTGTGGGAGATAGGCTCACATC	69
Db	45	ATCCAGATGACCGACGATCTCCATCTCCCTGTCTGCATCTGTGAGAGACAGATCACATC	104
Qy	70	ACCTGCGGCGCCAGCGAAACATCTATGCGCGCTGAACTGTATCAACGTAACCTGGG	129

Db	105	ACTGCGCGGGCAAGTCAGACGATTTAGCAGCTTTTAAATTGGTATTCAGACGAATATCAGG	164
Oy	130	AAAGCTCCGAGCCTTCTGATTTTACGCTGCAGCAACCTGGCAGATGAGTCCCTTCGC	189
Db	165	AAAGCCCCCTAACCTCTGATCTATCTGATCTGCATCCAGTTTCAAAATGAGGGTCCCATCAGG	224
Oy	190	TTCTCTGGATCCGGGCTCCGGAGCATTTTCACTTGACCATAGACATGTGAGGCTGAA	249
Db	225	TTTCAGTGGGAGTGGATCTGGGACATTTTCACTCTCCACATAGCAGTGTGACACTGAA	284
Oy	250	GACTTCGCTACCTATTAATCTAGCAACGTTTTTAAATTAATCTCCGTTGACTTTCGACAGGT	309
Db	285	GATTTTGGCACTACTTCTGCTGACGACGAGTTTCACTACACCCGCTAGACGTTTGGCCAGGG	344
Oy	310	ACCAAGGTGAAATAAAGCACTAGCTGGCGGTGGTGTCTG	349
Db	345	ACCAGACTGGAGATCAACGACTGTGGCTGCACCATCTG	384
RESULT	7		
LOCUS	AM406886	431 bp	EST
DEFINITION	UI-HF-BL0- <i>adg</i> -h-06-0-UI-r1 NIH_MGC_37 Homo sapiens cDNA clone		16-FEB-2000
ACCESSION	AM406886	IMAGE:3061499 5', mRNA sequence.	
VERSION	AM406886.1	GI:6925943	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 431)		
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	On Jan 6, 2000 this sequence version replaced gi:6675906. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbfp/image/image.html Seq primer: M13 Forward		
FEATURES	Location/Qualifiers		
Source	1..431		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:3061499"		
	/clone_1id="NIH_MGC_37"		
	/tissue_type="lymph"		
	/cell_type="germinal center B cells"		
	/cell_line="MGC85"		
	/lab_host="DH10 (LTI)"		
	/note="Vector: pRTT3-Pac; Site.1: NotI; Site.2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
BASE COUNT	101 a 125 c 105 g 100 t		
ORIGIN			
Query Match	24.5%	Score 183;	DB 72; Length 431;
Best Local Similarity	70.8%	Pred. NO. 5.2e-46;	
Matches 243;	Conservative	0; Mismatches 100;	Indels 0; Gaps 0;
7	CATATCCAGATGACCAAGTCCCGCTCTCCCTGTCGCGCTCTGTGGCGCATAGGCTACC	66	

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Db 60 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGTCATCTGTAGGAGACAGAGTCAC 119
QY 67 ATCACTTCGGCGGCGAGCGAAACATCTATGCGCGGCTGAACCTGTATCAACGTAAACCT 126
Db 120 ATCACTTCGGCGGCGAGTCAGAGCATTTAGCAGCTTTTAAATTTGATATCAGCAGAACCA 179
QY 127 GGGAAAGCTCCGAAGCTTCTGATTACGGTGGCGAGCAACCTTGGCAGATGGAGTCCCTTCT 186
Db 180 GGGAAAGCTCCGAAGCTTCTGATTACGGTGGCGAGCAACCTTGGCAGATGGAGTCCCTTCT 186
QY 187 GCGTTCCTGATCCGGTCCGGACGAGATTCACCTCTGACCATCAGCAGTCTGAGCCT 246
Db 240 AGGTTCAAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 299
QY 247 GAAGACTTCGCTAGCTATTTACTGTGACAGAACGTTTAAATATACCTTGTGACTTTGGGACAG 306
Db 300 GAAGATTTGCAACTTACTACTGTCAACAGAGTTACATACCCCTCGCATTTGGGGGA 359
QY 307 GGTACCAAGTGGAAATAAAACGTACTGCGGCTGGTGGTCTG 349
Db 360 GGGACCAAGTGGAGATCAACGAACCTGTGGCTGCACCATCTG 402

RESULT 8
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LOCUS UI-HF-BLO-abp-a-01-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3057288 5', mRNA sequence.
ACCESSION AW405752
VERSION AW405752.1 GI:6924809
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Aug 21, 1998 this sequence version replaced gi:3707751.
Contact: Robert Strausberg, Ph.D.
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M3 Forward.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_line="germinal center B cells"
/lab_host="DH10B (LT1)"
/notes="Vector: pT73-Pac; Site1: NotI; Site2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 105 a 129 c 111 g 102 t
ORIGIN
Query Match 24.5%; Score 183; DB 72; Length 447;
Best Local Similarity 70.8%; Pred. No. 5.3e-46;

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Matches 243; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
QY 7 GATATCCAGATGACCCAGTCCCGTCTCCCTGTGCGCTCTGTGGCGATAGGGTCACC 66
Db 83 GACATCCAGATGACCCAGTCTCGATCTCCCTGTGTCATCTGTAGGAGACAGTCACC 142
QY 67 ATCACTTCGGCGGCGAGCGAAACATCTATGCGCGCTGAACCTGGTATCAACGTAAACCT 136
Db 143 ATCACTTCGGCGGCGAGTCAAGCATTTAGCAGCTATTTAAATTTGATATCAGCAGACCA 202
QY 127 GGGAAAGCTCCGAAGCTTCTGATTACGGTGGCGAGCAACCTGCGCATGGAGTCCCTTCT 186
Db 203 GGGAAAGCTCCGAAGCTTCTGATTACGGTGGCGAGTTCACCTCTCACCATCAGCAGTCTGCAACCT 262
QY 187 GCGTTCCTGATCCGGTCCGGACGAGTTCACCTCTGACCATCAGCAGTCTGCGACCT 246
Db 263 ACCTTCAGTGGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 322
QY 247 GAAGACTTCGCTACGTATTACTGTCAAGAGCTTTTAAATATCTCCGTGACTTTGGGACAG 306
Db 323 GAAGATTTTGAACCTTACTACTGTCAACAGAGCTACAGTACCCCGTACAGTTTGGCCAG 382
QY 307 GGTACCAAGTGGAAATAAAACGTACTGCGGCTGGTGGTCTG 349
Db 383 GGGACCAAGTGGAGATCAACGAACCTGTGGCTGCACCATCTG 425

RESULT 9
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LOCUS UI-HF-BLO-acg-a-12-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3058847 5', mRNA sequence.
ACCESSION AW405906
VERSION AW405906.1 GI:6924963
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 460)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jul 8, 1999 this sequence version replaced gi:5422554.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M3 Forward.
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/cell_line="germinal center B cells"
/lab_host="DH10B (LT1)"
/notes="Vector: pT73-Pac; Site1: NotI; Site2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5Kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 107 a 128 c 113 g 112 t
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/lab_host="DH10B (LTI)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5Kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
98 a 108 c 94 g 91 t
BASE COUNT

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Query Match	24.1%	Score 179.8;	DB 72;	Length 391;
Best Local Similarity	71.9%;	Pred. No. 5e-45;		
Matches 235;	Conservative 0;	Mismatches 92;	Indels 0;	Gaps 0;

Qy	7	GATATCCAGATGACCCAGTCCCGCTCTCCCTGTCGCCCTCTGTGGCGATAGGTCACC	66
Db	65	GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGAGACAGAGTCACC	124
Qy	67	ATCACCTTCGGCGCGCCAGGAAACATCTATGGCGCGCTGAACTGGTATCAACGTTAAACCT	126
Db	125	ATCACTTCGGCGGCAAGTCAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAATCA	184
Qy	127	GGGAAAGCTCGGAAGCTTCTGATTACGGTCGGAGCAACCTGGCAGATGGAGTCCCTTCT	186
Db	185	GGGAAAGCCCTAAGCTCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCA	244
Qy	187	CGCTTCTCTGGATCCGCGCTCCGGACCGATTTCACTCTGACCATCAGCAGTCTCGAGCCT	246
Db	245	AGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT	304
Qy	247	GAAGACATTCGTACGTATTACTGTGCAGAACGTTTTTAAATACTCCGTTTGACTTTCGGACAG	306
Db	305	GAAGATTTGCAATTTACTACTGTTCAGCAGAGTTACAGTATCCCTCTCTACGTTTCGGCCAA	364
Qy	307	GGTACCAAGTGGAAATAAAACGCTACT	333
Db	365	GGGACCAAGTGGAAATCAAAACGAACT	391

RESULT	12
LOCUS	AW383563
LENGTH	453 bp
DEFINITION	mRNA EST O4-FEB-2000
ACCESSION	PM4-HT0348-261199-001-A07 HT0348 Homo sapiens cDNA, mRNA sequence.
VERSION	AW383563.1 GI:688131
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 453)
AUTHORS	HCGP http://www.ludwig.org.br/ORESTES .
TITLE	The FAPESP/LICR Human Cancer Genome Project
JOURNAL	Unpublished (1999)
COMMENT	On Jan 6, 2000 this sequence version replaced gi:6672417.

FEATURES
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 Location/Qualifiers
 High quality sequence stop: 452.
 Seq primer: puc 18 forward
 261199-001-A07&t3=1999-11-26&t4=1)
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&st2=PM4-HF0348-
 Project. This entry can be seen in the following URL
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Email: asimpson@ludwig.org.br
 Fax: +55-11-2707001
 Tel: +55-11-2704922
 Brazil

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/clone_lib="HT0348"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      108 a 125 c 107 g 113 t
ORIGIN

Query Match      24.1%; Score 179.8; DB 71; Length 453;
Best Local Similarity 70.3%; Pred. No. 5.2e-45;
Matches 241; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY  7  GATATCCAGATGACCCAGTCCCGTCTCCGTCTCCGTCTGTGGCGGATAGGGTCACC 66
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DB  71 GACATCCACATGACCCAGTCTCCATCCCGTCTCCGTCTGTGGCGGATAGGGTCACC 130
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QY  67 ATCACTCGGGCGCGACGGAAACATCTATGGCGCGCTGAACTGGTATCAACGTAACCT 126
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DB  131 ATCACTTTCGCGGCGAAGTCAGAGCATTAGTAGGTATTTAAATGGTATCAGCAGAAACCA 190
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QY  127 GGGAAAGCTCCGAAGCTTCTGATTACGGTGGCAGCAACCTGGCAGATGGAGTCCCTTCT 186
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DB  191 GGGAAAGCCCTCAGTTCCTGATCTATGCTGCATCTAGTTTGCAAGTGGGGTCCCAACA 250
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QY  187 CGCTCTCTGTGATCCGGTCCGGAAACGGATTCTACTCTGACCAATCAGAGTCTGCAGCCT 246
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DB  251 CGGTTCACTGAGTGGATCTGGCAGACAGTTCCTACTCTCACCATCAGCAGTCTGCAACCT 310
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QY  247 GAAGACTTCGTACGTATTACTGTCAGAACGTTTAAATACTCCGTTGACTTTCGGACAG 306
    || || || || || || || || || || || || || || || || || || || ||
DB  311 GAAGATTTCGAACCTTACTACTGTCACAGACTTATATACTACCCCTCGGACGTTTCGGCAA 370
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QY  307 GGTACCAAGTGGAAATAAACGTAAGTGGCGGTGGTGGTCTG 349
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DB  371 GGGACCAAGTGGAAATCAACGAAGTGTGGCTGCACCATCTG 413
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RESULT 13
AW403591
LOCUS      AW403591      488 bp      mRNA      EST      16-FEB-2000
DEFINITION UI-HF-BKO-abg-b-01-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056184 5', mRNA sequence.
ACCESSION  AW403591
VERSION     AW403591.1 GI:6922577
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE       NIH-MGC
JOURNAL     National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            ECO RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
            Location/Qualifiers
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                   /organism="Homo sapiens"

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DNA Sequencing by: M.B. Soares lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.dio.llnl.gov/bbrf/image/image.html
seq primer: M13 Forward.

Query Match	23.68%	Score 176.6	DB 72	Length 426
Best Local Similarity	69.78%	Pred. No. 5e-44		
Matches 239, Conservative	0	Mismatches 104	Indels 0	Gaps 0

BASE COUNT	111 a	111 c	99 g	105 t
ORIGIN				

Query Match	23.68;	Score 176.6;	DB 72;	Length 426;
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Best Local Similarity 69.7%; Pred. No. 5e-44;
Matches 239; Conservative 0; Mismatches 104; Indels 0; Gaps

7 GATATCCAGATGACCCAGTCCCGTCTCTCCCTGTCCGGCCTCTGTGGGCATAGGCTACC 66

Db 11 GACATCCAGATGACCCAGCTCTCCATCCTCCCTCTCTCTGCACTCTGTAGAGACAGAGATCACC 70

Oy 67 ATCACC TCGGCC CAGCGA AACAAT ATATGC CGCTGA ACTGTG ATCAAC GTAACT 126

Db 71 ATCACITGCCAGGCGAGTCAAGACATTAGCAAGIATTTAAATTGGTATCAGCAGAAACCA 130

127 GGGAAAGCTCCGAGCTTTCGATTACGGTGGCAGAACCTGGCAGATGGAGTCCCTTCT 186

187 GCGGAAAGCCCCCAAGCTCTGATCAGCATGCAACCAATTTGGAAACAGGGGTCCATCA 190

[illegible]

247 GAAGACTTCGCTACGATATTACTGTGCAGACCGTTTAAATACTCCGTTGACTTCGCGACAG 306

251 GAGATATTGCACATATTACTGTCAACAGTATGATAGTCTCCCCCTCACTTTCCGCGGA 3100

307 GGTACCAAGTGCAGTAATAAACGTAAGTGGCGGTGGTGGTTCTG 349

Db
311 GGGACCAAGTGGAGATCAACGACTGTGGCTGCACCATCTG 353

RESULT 15
AM406828
NW/066929
OGCS
1655 hr
EDNA
16-SEP-2000
DCM

LOCUS	400 bp	10 FEB 2000
DEFINITION	UT-HF-BLO- <i>adg-a-09-0-UT.r1</i> NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061169 5' mRNA sequence	ESI

ACCESSION	AM406828	1	GI:6925885
VERSION	AM406828.1	1	GI:6925885

KEYWORDS	EST.
SOURCE	human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi

REFERENCE
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 466)

AUTHORS NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
URL <http://www.ncbi.nlm.nih.gov/MGC/>

JOURNAL
unpublished (1999)
On Jan 6, 2000 this sequence version replaced g1:6675848.
COMMENT
Contact: Robert Strausberg ph D

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
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/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb) Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafide, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 109 a 125 c 116 g 116 t
ORIGIN

Query Match 23.6%; Score 176.6; DB 72; Length 466;
Best Local Similarity 69.7%; Pred. No. 5.1e-44;
Matches 239; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
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DB 45 GACATCCAGATGACCCAGTCTCTCCCTCCCTGCTCCGCTGTGGCGATAGGGTCACC 104
QY 67 ATCACCCTGCGCGCCAGCAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAACCT 126
DB 105 ATCATTGCGCGCCAGTACAGAGTGTAGTAGCTGGTGGCTGGTATCAGCAGAACCA 164
QY 127 GGGAAAGCTCCGAAGCTTCTGATTTAGCGTGGCGAGCAACCTGGCAGATGGAGTCCCTTCT 186
DB 165 GGGAAAGCTTAACTGCTGATCTATAAGCGCTAGTTAGAAAGTGGGTCCCATCA 224
QY 187 CGCTTCTCTGATCCGCTCCGGAACGATTCACCTGACCATCAGCAGTCTGCAGCCT 246
DB 225 AGATTACGCGCAGTGGATCTGGGACAGAAATTCACCTCACCATCAGCAGCCTGCAGCCT 284
QY 247 GAAGACTTCGCTACGTATTACTGTGAGAACGTTTAAATACCTCCGTTGACTTTGGGACAG 306
DB 285 GATGATTTGCACTTATTACTGCAACAGTATTAATAGTTACCCCTGGACGTTTGGCAA 344
QY 307 GGTACCAAGGTGGAATAAAGTACTGGCGGTGGTGGTCTG 349
DB 345 GGGACCAAGGTGGAATAAAGTACTGGCGGTGGTGGTCTG 387

Search completed: September 12, 2000, 20:04:48
Job time: 3485 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 20:01:31 ; Search time 73.77 Seconds

(without alignments)
2533.462 Million cell updates/sec

Title: US-08-487-283a-8

Perfect score: 747
Sequence: 1 ATGGCCGATATCCAGATGAC.....TGGTCACGTCTCGAGCTGA 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 segs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	747	100.0	747	1	T08480 Humanised CDR-graft
2	729.4	97.6	747	1	T08488 Humanised CDR-graft
3	396.6	53.1	747	1	T08479 Murine 5G1.1M1 scf
4	371	49.7	750	1	T08484 Humanised 5G1.1 VH
5	358.2	48.0	750	1	T08487 Humanised 5G1.1 VH
6	350.2	46.9	750	1	T08483 Humanised 5G1.1 VH
7	328.8	44.0	726	1	T110706 Humanised 5G1.1 VL
8	323.8	43.3	711	1	T08486 Humanised 5G1.1 VL
9	322.4	43.2	726	1	T08485 Humanised 5G1.1 VL
10	294	39.4	819	1	O20381 Sequence encoding
11	283.4	37.9	723	1	O42284 V-J(kappa)/((Gly)4
12	267	35.7	1065	1	T94563 R. pipliens recombi
13	267	35.7	1065	1	T94567 R. pipliens recombi
14	267	35.7	1074	1	T94965 R. pipliens recombi
15	267	35.7	1074	1	T94968 R. pipliens recombi
16	267	35.7	1086	1	T94966 R. pipliens recombi
17	267	35.7	1137	1	T94964 R. pipliens recombi
18	250	33.5	729	1	O73679 Fv(Gp-4) Immunosp
19	249.2	33.4	783	1	Anti-C5 Mab N19/8
20	247.2	33.1	913	1	O81076 Bispecific CD3-L6F
21	239.6	32.1	1149	1	T90514 DNA encoding chime
22	239.6	32.1	1212	1	T90511 DNA encoding chime
23	239.6	32.1	1422	1	T90509 DNA encoding chime
24	239.6	32.1	1545	1	T90510 DNA encoding chime
25	239.6	32.1	1956	1	T90512 DNA encoding chime
26	239.6	32.1	2079	1	T90513 DNA encoding chime
27	236.6	31.7	733	1	V99766 A33/218 single-cha
28	236.6	31.7	1938	1	V58929 A33 chimeric recep
29	234.4	31.4	721	1	V99765 A33/212 single-cha
30	232.8	31.2	720	1	T91615 cDNA encoding an a
31	232.4	31.1	2178	1	O25592 Encodes 4D5 Fab Ig
32	232.4	31.1	2178	1	V81689 4D5 Fab molecule e
33	231.6	31.0	5227	1	T79537 Plasmid pTERMSC2H1

34	231	30.9	6727	1	V63616 Nucleic acid seque
35	230.6	30.9	1299	1	V63620 Nucleic acid seque
36	230.6	30.9	1320	1	V63617 Nucleic acid seque
37	230.6	30.9	6799	1	V63619 Nucleic acid seque
38	227.6	30.5	2143	1	X03840 Plasmid pS1130 exp
39	227	30.4	735	1	T91614 cDNA encoding an a
40	224.8	30.1	819	1	T35691 Nematode salivary
41	224.8	30.1	819	1	T86646 Mus musculus antib
42	224.4	30.0	732	1	O73678 Fv(Gp-2) Immunosp
43	223.2	29.9	6127	1	X07474 Mus musculus anti-
44	221.8	29.7	720	1	O55181 Sequence encoding
45	221.8	29.7	720	1	T65007 Single-chain anti-

ALIGNMENTS

RESULT	ID	Query Match	Score	DB 1:	Length	747:	Mismatches	0:	Indels	0:	Gaps	0:
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T08480	1	100.0%	747	1	747							
AC	T08480:	100.0%	747	1	747							
DT	15-MAR-1996 (first entry)	100.0%	747	1	747							
DE	Humanised CDR-grafted 5G1.1 scFv CB DNA.	100.0%	747	1	747							
KW	Complement C5; haemolysis; kidney; glomerulonephritis;	100.0%	747	1	747							
KW	monoclonal antibody; antiinflammatory; antibody engineering;	100.0%	747	1	747							
KW	humanised antibody; complementarity determining region; CDR;	100.0%	747	1	747							
OS	single chain antibody; scfv; ds.	100.0%	747	1	747							
FT	Synthetic.	100.0%	747	1	747							
FT	Key	100.0%	747	1	747							
FT	cds	100.0%	747	1	747							
PN	WO9529697-A1.	100.0%	747	1	747							
PD	09-NOV-1995.	100.0%	747	1	747							
PR	01-MAY-1995; U05688.	100.0%	747	1	747							
PR	02-MAY-1994; US-236208.	100.0%	747	1	747							
PA	(ALEX-) ALEXION PHARM INC.	100.0%	747	1	747							
PI	Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;	100.0%	747	1	747							
PI	Rother RP, Springhorn J P, Squinto SP, Thomas TC;	100.0%	747	1	747							
PI	Wang Y, Wilkins JA;	100.0%	747	1	747							
DR	WPI: 95-392923/50.	100.0%	747	1	747							
DR	P-PSDB: R77607.	100.0%	747	1	747							
PT	Treating glomerulonephritis with antibody against complement C5	100.0%	747	1	747							
PS	component - to inhibit complement induced cell lysis	100.0%	747	1	747							
PS	Claim 33: Page 110-113; 181pp; English.	100.0%	747	1	747							
CC	DNA (T08480) coding for humanised CDR-grafted scfv CB (R77607) was	100.0%	747	1	747							
CC	derived from DNA of hybridoma ATCC HB 11625, the producer of anti-C5	100.0%	747	1	747							
CC	monoclonal antibody (Mab) 5G1.1. The DNA was subcloned into vector	100.0%	747	1	747							
CC	PER Ttc S05/NI for expression in Escherichia coli. The light and/or	100.0%	747	1	747							
CC	heavy chain CDRs of scfv CB can be combined with CDRs from other	100.0%	747	1	747							
CC	5G1.1-derived antibodies, Fds and light chains (R77607-16) in the	100.0%	747	1	747							
CC	prodn. of recombinant, including humanised, antibodies that retain	100.0%	747	1	747							
CC	the ability of Mab 5G1.1 to block human complement C5a generation	100.0%	747	1	747							
CC	and thus to reduce glomerular inflammation and kidney dysfunction	100.0%	747	1	747							
CC	associated with glomerulonephritis.	100.0%	747	1	747							
Sequence	747 BP; 161 A; 186 C; 209 G; 191 T;	100.0%	747	1	747							
Query Match	100.0%; Score 747; DB 1: Length 747;	100.0%	747	1	747							
Best Local Similarity	100.0%; Pred. No. 5.7e-199;	100.0%	747	1	747							
Matches	747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%	747	1	747							
OY	1 ATGGCCGATATCCAGATGACCCCGTCCCTGTCGCGCTGTGGCGCATAGG 60	100.0%	747	1	747							
DB	1 ATGGCCGATATCCAGATGACCCCGTCCCTGTCGCGCTGTGGCGCATAGG 60	100.0%	747	1	747							
OY	61 GTACACATACCTGGGCGCCAGCAAAACATCTATGGCGCGCTGACATGATCAAGT 120	100.0%	747	1	747							
DB	61 GTACACATACCTGGGCGCCAGCAAAACATCTATGGCGCGCTGACATGATCAAGT 120	100.0%	747	1	747							
OY	121 AAACCTGGGAAGCTCCGAAGCTTGTATGATGCGACGACCACTGCGACATGAGT 180	100.0%	747	1	747							
DB	121 AAACCTGGGAAGCTCCGAAGCTTGTATGATGCGACGACCACTGCGACATGAGT 180	100.0%	747	1	747							
OY	181 CCTTCTGCTCTGTGATCGGCTCCGACGAGATTACTCTACATCAGCAGTCTG 240	100.0%	747	1	747							
DB	181 CCTTCTGCTCTGTGATCGGCTCCGACGAGATTACTCTACATCAGCAGTCTG 240	100.0%	747	1	747							

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241	Db	 CAGCCCTGAGAGACTTCGCTACGTATTACTGTCAGAAGCTTTTAAATACTCGCTTGACTTTC	300
301	QY	 GGACAGGCTACCAAGGTGGAAATAAAACGTACTGCGCGTGGTGGTTCTGGTGGCGGCTGGA	360
301	Db	 GGACAGGCTACCAAGGTGGAAATAAAACGTACTGCGCGTGGTGGTTCTGGTGGCGGCTGGA	360
361	QY	 TCTGTGGTGGCGGTTTCTCAAGTCCAACTGGTGCAAATCCGGCGCCGAGTCAAGAAGCCA	420
361	Db	 TCTGTGGTGGCGGTTTCTCAAGTCCAACTGGTGCAAATCCGGCGCCGAGTCAAGAAGCCA	420
421	QY	 GGGGCCTCAGTCAAAGTGTCCTGTAAGCTAGCGGCTATATTTTTTCTTAATTATTGGATT	480
421	Db	 GGGGCCTCAGTCAAAGTGTCCTGTAAGCTAGCGGCTATATTTTTTCTTAATTATTGGATT	480
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541	Db	 TCTGCTAGCACCGAAATATACCGAAAATTTTAAAGACCGTGTACTATGACGCGTGACACT	600
601	QY	 TCGACTAGTACAGTATACATGGAGCTCTCCAGCCTCGGATCGGAGGACACGGCCGCTAT	660
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661	QY	 TATTGGCGCGTTATTTTTTTGGTTCTAGCCCGAATTTGGTATTTTGGGTCTAA	720
661	Db	 TATTGGCGCGTTATTTTTTTGGTTCTAGCCCGAATTTGGTATTTTGGGTCTAA	720
721	QY	 GGAAACCTTGGTCACTGCTCGAGCTGA	747
721	Db	 GGAAACCTTGGTCACTGCTCGAGCTGA	747

RESULT 2

T08488	T08488 standard; DNA; 747 BP.
AC	T08488;
ID	T08488;
DE	15-MAR-1996 (first entry)
DE	Humanised CDR-grafted 5G1.1 scFv D012 DNA.
DE	Complement C5; haemolysis; kidney; glomerulonephritis;
KW	monoclonal antibody; antiinflammatory; antibody engineering;
KW	humanised antibody; complementarity determining region; CDR;
KW	single cell antibody; scFv; ds.
OS	Synthetic.
FT	Key
FT	Location/Qualifiers
FT	1. 747
FT	/*tag= a
FT	WO9529697-A1.
PN	09-NOV-1995.
PF	01-NOV-1995; U05688.
PF	02-MAY-1994; US-236208.
PR	(ALEX-) ALEXION PHARM INC.
PR	Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI	Rothery RP, Springhorn J P, Squinto SP, Thomas TC;
PI	Wang Y, Wilkins JA;
PI	WPI: 95-392923/50.
DR	P-PSDB; R77616.
DR	Treating glomerulonephritis with antibody against complement C5
PT	component - to inhibit complement induced cell lysis
PT	Claim 34; Page 138-140; 181pp; English.
BS	A DNA construct (T08488) codes for a humanised CDR-grafted
CC	scFv, designated 5G1.1 scFv D012 (R77616), which includes
CC	CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.
CC	DNA can be subcloned into vector pET Trc S05/N1 (see T08489) for
CC	expression of humanised scFv in Escherichia coli M61 cells. The
CC	recombinant antibodies retain the ability of MAB 5G1.1 to block

OS Mus sp. Location/Qualifiers
 FH Key 1.747
 FT cds /*tag= a
 PN WO9529697-A1.
 PD 09-NOV-1995.
 PF 01-MAY-1995; U05688.
 PR 02-MAY-1994; US-236208.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 DR WPI: 95-392923/50.
 DR P-PSDB: R77606.
 PT Treating glomerulonephritis with antibody against complement C5
 PS Claim 24: Page 107-110, 181pp; English.
 CC DNA (T08484/9) coding for murine scFv 5G1.1M1 (R77606) was obtd. by
 CC PCR cloning of DNA from hybridoma ATCC HB 11623, the producer of
 CC anti-C5 monoclonal antibody (Mab) 5G1.1. The DNA was subcloned into
 CC pET-30(+/-) for expression in Escherichia coli. The light and/or
 CC heavy chain CDRs of scFv 5G1.1M1 can be combined with CDRs from other
 CC 5G1.1-derived antibodies, Fds and light chains (R77607-16) in the
 CC prodn. of recombinant, including humanised, antibodies that retain
 CC the ability of Mab 5G1.1 to block human complement C5a generation
 CC and thus to reduce glomerular inflammation and kidney dysfunction
 CC associated with glomerulonephritis.
 SO Sequence 747 BP; 183 A; 174 C; 211 G; 179 T;

Query Match 53.1%; Score 396.6; DB 1; Length 747;
 Best Local Similarity 70.7%; Pred. No. 2e-101;
 Matches 528; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

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 1 ATGGCCGATATTCAGATATACCAAGCCCGCTCTCCCTCTGGCCGATAG 60
 DB 1 ATGGCCGATATTCAGATATACCAAGCCCGCTCTCCCTCTGGCCGATAG 60
 QY 61 GTCACATCAGCTGGGGCCGAGCAAAACATCTATGGCGCTGATCAACGT 120
 61 GTCACATCAGCTGGGGCCGAGCAAAACATCTATGGCGCTGATCAACGT 120
 DB 61 GTCACATCAGCTGGGGCCGAGCAAAACATCTATGGCGCTGATCAACGT 120
 QY 121 AAACCTGGGAAAGCTCCGAAAGCTTCTGATTTAGGTCGACAGCACTGGCAGTGC 180
 121 AAACCTGGGAAAGCTCCGAAAGCTTCTGATTTAGGTCGACAGCACTGGCAGTGC 180
 DB 121 AAACCTGGGAAAGCTCCGAAAGCTTCTGATTTAGGTCGACAGCACTGGCAGTGC 180
 QY 181 CCTTCTCCCTCTCTGATTCGCGCTCCGAGCAGATTTCACTGACATCAGCAGTCTG 240
 181 CCTTCTCCCTCTCTGATTCGCGCTCCGAGCAGATTTCACTGACATCAGCAGTCTG 240
 DB 181 CCTTCTCCCTCTCTGATTCGCGCTCCGAGCAGATTTCACTGACATCAGCAGTCTG 240
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 DB 301 GGACAGGGTACCAAGAGTGGATAAATAAGTACTGGCGGTGTCTGTCGGCGGTGA 360
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 DB 361 TCTGGTGTGGCGGTCTCAAGTCTCAAGTCTGATCGGCGCGGAGGTCAAGAACCA 420
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 DB 541 TCTGTATACCAAGATATACGAAATTTTAAAGACCGTGTACTATGACGGGTGACACT 600

QY 601 TCGACTAGTACAGTATACATGAGACTCTCCAGCTCGGATCGGAGACAGCCGCTAT 660
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 721 GGAACCTGGTCACTGCTCGAGCTGA 747
 DB 721 GGAACCTGGTCACTGCTCGAGCTGA 747

RESULT 4
 ID T08484 standard; DNA: 750 BP.
 AC T08484;
 DT 02-APR-1996 (first entry)
 DE Humanised 5G1.1 VH + IGHRLC DNA.
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarily determining region; CDR;
 OS ds.
 FH Key
 FT cds 1.750
 FT signal_peptide 1.57
 FT mat_peptide 58.747
 FT mat_peptide /*tag= c
 PN WO9529697-A1.
 PD 09-NOV-1995.
 PE 01-MAY-1995; U05688.
 PR 02-MAY-1994; US-236208.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 DR WPI: 95-392923/50.
 DR P-PSDB: R77611.
 PT Treating glomerulonephritis with antibody against complement C5
 PS Claim 38: Page 123-125, 181pp; English.
 CC A DNA construct (T08483) codes for a humanised CDR-grafted and
 CC framework sequence-altered Fd 5G1.1 VH + IGHRLC (R77610), which
 CC includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.
 CC The DNA can be subcloned together with DNA (T08484) coding for a
 CC humanised light chain (R77612) into vector ALEX-3P (T08476) for
 CC expression of humanised antibody in human 293 EBNA cells. Such
 CC recombinant antibodies retain the ability of Mab 5G1.1 to block
 CC human complement C5a generation and thus to reduce glomerular
 CC inflammation and kidney dysfunction associated with
 CC glomerulonephritis.
 SO Sequence 750 BP; 163 A; 220 C; 197 G; 170 T;

Query Match 49.7%; Score 371; DB 1; Length 750;
 Best Local Similarity 97.4%; Pred. No. 2.7e-94;
 Matches 377; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 358 GGATCTGGTGGTGGCGGTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 417
 358 GGATCTGGTGGTGGCGGTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 417
 DB 358 GGATCTGGTGGTGGCGGTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 417
 QY 37 GTAAGTGGCGCGCTCCAGTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 96
 37 GTAAGTGGCGCGCTCCAGTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 96
 DB 37 GTAAGTGGCGCGCTCCAGTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 96
 QY 418 CAGGAGGCTTCAATCAAGTCTCTGTAAGCTAGCGGCTATATTTTATATATG 477
 418 CAGGAGGCTTCAATCAAGTCTCTGTAAGCTAGCGGCTATATTTTATATATG 477
 DB 418 CAGGAGGCTTCAATCAAGTCTCTGTAAGCTAGCGGCTATATTTTATATATG 477
 QY 478 ATTCATAGGTGGTGAAGCGCGCGGAGGCGCTGGAATGAGTGGTGAATCTTACCG 537
 478 ATTCATAGGTGGTGAAGCGCGCGGAGGCGCTGGAATGAGTGGTGAATCTTACCG 537
 DB 478 ATTCATAGGTGGTGAAGCGCGCGGAGGCGCTGGAATGAGTGGTGAATCTTACCG 537
 QY 537 ATTCATAGGTGGTGAAGCGCGCGGAGGCGCTGGAATGAGTGGTGAATCTTACCG 537
 DB 537 ATTCATAGGTGGTGAAGCGCGCGGAGGCGCTGGAATGAGTGGTGAATCTTACCG 537

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QY 538 GGCTCTGTAGCACCAGATATACCGAAATTTTAAAGACCGGTGTACTATGACGGTGAC 597
|||||
Db 217 GGCTCTGTAGCACCAGATATACCGAAATTTTAAAGACCGGTGTACTATGACGGTGAC 276
|||||
QY 598 ACTTCGACTAGTACAGTATACATGAGAGCTCTCCAGCCCTGCGATCGGAGGACACGCGCGTC 657
|||||
Db 277 ACTTCGACTAGTACAGTATACATGAGAGCTCTCCAGCCCTGCGATCGGAGGACACGCGCGTC 336
|||||
QY 658 TATTATTGCGCGCGGTATTATTTTGGTCTAGCCCGAATTTGGTATTGATGTTGGGGT 717
|||||
Db 337 TATTATTGCGCGCGGTATTATTTTGGTCTAGCCCGAATTTGGTATTGATGTTGGGGT 396
|||||
QY 718 CAAGGAACCCCTGGTCACTGTCTCGAGC 744
|||||
Db 397 CAAGGAACCCCTGGTCACTGTCTCGAGC 423
|||||

RESULT 5
T08487
ID T08487 standard; DNA; 750 BP.
AC T08487;
DE 02-APR-1996 (first entry)
KW Humanised 5G1.1 VH + IGHRLD DNA.
KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW ds.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 1..750
FT signal_peptide 1..57
FT mat_peptide 58..747
FT WO9529697-A1.
FT 09-NOV-1995.
FT 01-MAY-1995; U05688.
FT 02-MAY-1994; US-236208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
PI WPI: 95-392923/50.
DR P-PSDB; R77615.
DR Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS Claim 37: Pages 135-137; 181pp; English.
CC A DNA construct (T08487) codes for a humanised CDR-grafted
CC light chain, designated 5G1.1 VL + IGHRLD (R77615), which includes
CC CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The
CC DNA can be subcloned together with DNA (T08484) coding
CC for a humanised Fd (R77611) into vector APEX-3P (T08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of Mab 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
SQ Sequence 750 BP; 160 A; 223 C; 198 G; 169 T;

Query Match 48.0%; Score 358.2; DB 1; Length 750;
Best Local Similarity 95.3%; Pred. No. 9.8e-91;
Matches 369; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 358 GGATCTGGTGGCGGTCTCAAGTCCAACTGGTCAACTCGCGCCGAGGTCAAGAAG 417
|||||
Db 37 GTAATCGCGCGGTCCACATCCCAAGTCCAACTGGTCAACTCGCGCCGAGGTCAAGAAG 96
|||||
QY 418 CCAGGGGCGCTCAGTCAAAGTGCTCTAAAGCTAGCGGCTATATTTTCTAATTATTGG 477
|||||
Db 97 CCAGGGGCGCTCAGTCAAAGTGCTCTAAAGCTAGCGGCTATATTTTCTAATTATTGG 156
|||||
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QY 478 ATTCAATGGTGGTCCAGGCCCGCCGAGGCGCTGGAATGGATGGGTGAGATCTTACCG 537
|||||
Db 157 ATTCAATGGTGGTCCAGGCCCGCCGAGGCGCTGGAATGGATGGGTGAGATCTTACCG 216
|||||
QY 538 GGCTCTGTAGCACCAGATATACCGAAATTTTAAAGACCGGTGTACTATGACGGTGAC 597
|||||
Db 217 GGCTCTGTAGCACCAGATATACCGAAATTTTAAAGACCGGTGTACTATGACGGTGAC 276
|||||
QY 598 ACTTCGACTAGTACAGTATACATGAGAGCTCTCCAGCCCTGCGATCGGAGGACACGCGCGTC 657
|||||
Db 277 ACTTCGACTAGTACAGTATACATGAGAGCTCTCCAGCCCTGCGATCGGAGGACACGCGCGTC 336
|||||
QY 658 TATTATTGCGCGCGGTATTATTTTGGTCTAGCCCGAATTTGGTATTGATGTTGGGGT 717
|||||
Db 337 TATTATTGCGCGCGGTATTATTTTGGTCTAGCCCGAATTTGGTATTGATGTTGGGGT 396
|||||
QY 718 CAAGGAACCCCTGGTCACTGTCTCGAGC 744
|||||
Db 397 CAAGGAACCCCTGGTCACTGTCTCGAGC 423
|||||

RESULT 6
T08483
ID T08483 standard; DNA; 750 BP.
AC T08483;
DT 15-MAR-1996 (first entry)
DE Humanised 5G1.1 VH + IGHRL DNA.
KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW ds.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 1..750
FT signal_peptide 1..57
FT mat_peptide 58..747
FT WO9529697-A1.
FT 09-NOV-1995.
FT 01-MAY-1995; U05688.
FT 02-MAY-1994; US-236208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
PI WPI: 95-392923/50.
DR P-PSDB; R77610.
DR Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS Claim 42: Page 119-122; 181pp; English.
CC A DNA construct (T08483) codes for a humanised CDR-grafted and
CC framework sequence-altered Fd 5G1.1 VH + IGHRL (R77610), which
CC includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.
CC The DNA can be subcloned together with DNA (T08484) coding for a
CC humanised light chain (R77612) into vector APEX-3P (T08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of Mab 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
SQ Sequence 750 BP; 159 A; 225 C; 199 G; 167 T;

Query Match 46.9%; Score 350.2; DB 1; Length 750;
Best Local Similarity 94.1%; Pred. No. 1.6e-98;
Matches 364; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 358 GGATCTGGTGGCGGTCTCAAGTCCAACTGGTCAACTCGCGCCGAGGTCAAGAAG 417
|||||
Db 37 GTAATCGCGCGGTCCACATCCCAAGTCCAACTGGTCAACTCGCGCCGAGGTCAAGAAG 96
|||||
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Oy	418	CCAGGGGCGCTAGTCAAGAGTGCTCCTGTAACCTGACGGCTATATTTTCTTAATTATGG	477
Db	97	CCAGGGGCGCTAGTCAAGAGTGCTCCTGTAACCTGACGGCTATATTTTCTTAATTATGG	156
Oy	478	ATTCAAATGGGTGCTGCAGAGCCCCGGGCGAGGCGCTGGAATGGATGGGTGAGATCTTACCG	537
Db	157	ATTCAAATGGGTGCTGCAGAGCCCCGGGCGAGGCGCTGGAATGGATGGGTGAGATCTTACCG	216
Oy	538	GGCCTCTGTGCTACACCGAATATACGAAATTTTAAAGACCGTGTACTATGACCGCGTGAC	597
Db	217	GGCTCTGTGCTACACCGAATATGCCCCAAATTTCAAGGCGCGTGTACTATGACCTGCGGAC	276
Oy	598	ACTTCGACTAGTACAGTATACATGAGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTC	657
Db	277	ACTTCGACTAGTACAGCCTTACATGAGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTC	336
Oy	658	TATTAATGCGGCGGTATATTTTGGTTCCTAGCCCGAATGGTATTTTGATGTTGGGGT	717
Db	337	TATTAATGCGGCGGTATATTTTGGTTCCTAGCCCGAATGGTATTTTGATGTTGGGGT	386
Oy	718	CAAGGAACCTGATGACATGTCGAGC	744
Db	387	CAAGGAACCTGATGACATGTCGAGC	423

Query Match	Best Local Similarity	Score	DB 1:	Length	726:
Matches 336;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;	

QY 2 TGCCCGATATCCAGATGACGACCCAGTCCCGCTCTCCCTGTCCGGCTCTGTGTGGGCGATATAGGG 61

Db 77 TGCAGGATATCCAGATGACCCAGTCCCGCTCTCTCTGTCCGCTCTGTGTGGGCGATATAGGG 136

QY 62 TCACCATCATCCGCGGGCCGACGAGAAACATCTATGGGCGGCTCACTACGTGGATATACGTA 121

Db 137 TCACCATCATCTCGCGGCCCGACGCGAAACATCTATGGGCGGCTCACTACGTGGATATACGTA 196

QY 122 AACCTGGGAAAGCTCCGAGCTTCTGATTACGGGTGCGACCAACCTGGCAGATGAGATCC 181

Db 197 AACCTGGGAAAGCTCCGAGCTTCTGATTACGGGTGCGACCAACCTGGCAGATGAGATCC 256

QY 182 CTCTCGCTCTCTGTGATCCGGCTCCGGAGACGATTCACCTGACCATCAGCAGTCTGC 241

Db 257 CTCTCGCTCTCTGTGATCCGGCTCCGGAGACGATTCACCTGACCATCAGCAGTCTGC 316

QY 242 AGCTTGAAGACTTGCGCTACGATTACTGTCAGAACGTTTAAATACCTCCGTGACTTTG 301

Db 317 AGCCCTGAAGACTTGCGCTACGATTACTGTCAGAACGTTTAAATACCTCCGTGACTTTG 376

QY 302 GACGAGGTACCAAGGTGGAATTAACGTAACGTAATGGCGGGGTGTCTG 349

Db 377 GACGAGGTACCAAGGTGGAATTAACGTAACGTAATGGCGGGGTGTCTG 424

RESULT	8	
T08486		
T08486 standard; DNA; 711 BP.		
AC	T08486;	
DE	15-MAR-1996 (first entry)	
DE	Humanised 5G1.1 VL + 012 DNA.	
KM	Complement C5; haemolysis; kidney; glomerulonephritis;	
KM	monoclonal antibody; antiinflammatory; antibody engineering;	
KM	humanised antibody; complementarity determining region; CDR;	
OS	ds.	
OS	Synthetic.	
PM	Key	Location/Qualifiers
FT	cds	1..711
FT		/*tag= a
FT	signal_peptide	1..66
FT		/*tag= b
FT	mat_peptide	67..708
FT		/*tag= C
PN	WO9529697-A1.	
PN	09-NOV-1995.	
PR	01-MAY-1995; U05688.	
PR	02-MAY-1994; US-236208.	
PA	(ALEX-) ALEXION PHARM INC.	
PI	Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;	
PI	Rother RP, Springhorn J P, Squinto SP, Thomas TC;	
PI	Wang Y, Wilkins JA;	
DR	WPI: 95-392923/50.	
DR	P-PsDB: R77614.	
PT	Treating glomerulonephritis with antibody against complement C5	
PT	component - to inhibit complement induced cell lysis	
PS	Claim 35; Page 132-34; 181pp; English.	
CC	A DNA construct (T08486) codes for a humanised CDR-grafted	
CC	light chain, designated 5G1.1 VL + 012 (R77614), which includes	
CC	CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The	
CC	DNA can be subcloned together with DNA (T08484) coding	
CC	for a humanised Fd (R77611) into vector APEX-3p (T08476) for	
CC	expression of humanised antibody in human 293 EBNA cells. Such	
CC	recombinant antibodies retain the ability of Mab 5G1.1 to block	
CC	human complement C5a generation and thus to reduce glomerular	
CC	inflammation and kidney dysfunction associated with	
CC	glomerulonephritis.	
SQ	Sequence 711 BP;	174 A; 206 C; 183 G; 148 T;
Query Match	43.3%;	Score 323.8; DB 1; Length 711;
Best Local Similarity	96.5%;	Pred. No. 3.6e-81;
Matches 331; Conservative	0;	Mismatches 12; Indels 0; Gaps 0;


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QY 7 GATATCCAGATGACCCAGTCCCGTCCCTCTGTCGGCGATAGGTCACC 66
  |||
Db 67 GATATCCAGATGACCCAGTCCCGTCCCTCTGTCGGCGATAGGTCACC 126
  |||
QY 67 ATCACTGGCGCGCCAGCAAAACATCTATGGCGGCTGAACCTGTATCAACGTAACCT 126
  |||
Db 127 ATCACTGGCGCGCCAGCAAAACATCTATGGCGGCTGAACCTGTATCAACGTAACCT 186
  |||
QY 127 GGGAAAGCTCCGAAGCTTCGATTACGGTGGGAGCAACCTGGCAGATGGAGTCCCTTCT 186
  |||
Db 187 GGGAAAGCTCCGAAGCTTCGATTACGGTGGGAGCAACCTGGCAGATGGAGTCCCTTCT 246
  |||
QY 187 CGCTTCTCTGGATCCGGTCCCGGAACGATTTCACTCTGACCATCAGCAGTCTGCAGCT 246
  |||
Db 247 CGCTTCTCTGGATCCGGTCCCGGAACGATTTCACTCTGACCATCAGCAGTCTGCAGCT 306
  |||
QY 247 GAAGACTTCGCTAGCTATTACTGTGACAAAGCTTTTAAATACCTCCGTTTCGGACAG 306
  |||
Db 307 GAAGACTTCGCTAGCTATTACTGTGACAAAGCTTTTAAATACCTCCGTTTCGGACAG 366
  |||
QY 307 GGTACCAAGGTGGAAATAAAGCACTGGCGGTGGTGGTCTTG 349
  |||
Db 367 GGTACCAAGGTGGAAATAAAGCACTGGCGTGCACCATCTG 409
  |||
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RESULT 9

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T08485
ID T08485 standard; DNA; 726 BP.
AC T08485;
DT 15-MAR-1996 (first entry)
DE Humanised 5G1.1 VL + KLV56 DNA.
KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW ds.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 1..726
FT signal_peptide 1..75 /*tag= a
FT mat_peptide 76..723 /*tag= b
FT mat_peptide 76..723 /*tag= c
PN WO9529697-A1.
PD 09-NOV-1995.
PF 01-MAY-1995; U05688.
PR 02-MAY-1994; US-236208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
PI WPI; 95-392923/50.
DR P-PSDB; T08485.
DR Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS Example 11: Page 126-128; 181pp; English.
CC A DNA construct (T08485) codes for a humanised CDR-grafted and
CC framework sequence-altered light chain, 5G1.1 VL + KLV56 (R77612),
CC which includes CDRs derived from mouse anti-C5 monoclonal antibody
CC 5G1.1. The DNA can be subcloned together with DNA (T08483) coding
CC for a humanised Fd (R77610) into vector APEX-3P (T08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of MAb 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
SQ Sequence 726 BP; 176 A; 207 C; 186 G; 157 T;

Query Match 43.2%; Score 322.4; DB 1; Length 726;
Best Local Similarity 95.4%; Pred. No. 8.9e-81;
Matches 332; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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QY 2 TGGCCGATATCCAGATGACCCAGTCCCGTCCCTCTGTCGGCGATAGG 61
  |||
Db 77 TGCAGGATATCCAGATGACCCAGTCCCGTCCCTCTGTCGGCGATAGG 136
  |||
QY 62 TCACCATCACTTCGCGCGCCAGCAAAACATCTATGGCGGCTGAACCTGTATCAACGTA 121
  |||
Db 137 TCACCATCACTTCGCGCGCCAGCAAAACATCTATGGCGGCTGAACCTGTATCAACGTA 196
  |||
QY 122 AACCTGGGAAAGCTCCGAAGCTTCGATTACGGTGGGAGCAACCTGGCAGATGGAGTCC 181
  |||
Db 197 AACCTGGGAAAGCTCCGAAGCTTCGATTACGGTGGGAGCAACCTGGCAGATGGAGTCC 256
  |||
QY 182 CTTCTCTCTCTCTGATCCGGTCCCGGAACGATTTCACTCTGACCATCAGCAGTCTGC 241
  |||
Db 257 CTTCTCTCTCTCTGATCCGGTCCCGGAACGATTTCACTCTGACCATCAGCAGTCTGC 316
  |||
QY 242 AGCCTGAAGACTTCGCTAGCTATTACTGTGACAAAGCTTTTAAATACCTCCGTTGACTTTCG 301
  |||
Db 317 AACCTGAGGACTTCGCTAGCTATTACTGTGACAAAGCTTTTAAATACCTCCGTTGACTTTCG 376
  |||
QY 302 GACAGGTACCAAGGTGGAAATAAAGCACTGGCGGTGGTGGTCTTG 349
  |||
Db 377 GACAGGTACCAAGGTGGAAATAAAGCACTGGCGTGCACCATCTG 424
  |||
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RESULT 10

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Q20381
ID Q20381 standard; DNA; 819 BP.
AC Q20381;
DT 15-APR-1992 (first entry)
DE Sequence encoding the shortened hinge version of the B72.3 single
DE chain Fv hinge.
KW Fv fragment; in vivo diagnosis; therapy; antibody; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..816
FT /*tag= a
PN WO9119739-A.
PD 26-DEC-1991.
PF 11-JUN-1991; G00935.
PR 11-JUN-1990; GB-012995.
PA (CELL-) CELLSOURCE LTD.
PI King DJ, Mountain A, Owens RJ, Yarranton GT;
PI WPI; 92-024365/03.
DR P-PSDB; R20185.
DR New multivalent antigen-binding proteins - comprise Fv fragment
PT linked to at least 1 other Fv fragment spacer and useful for
PT in-vivo diagnosis or therapy
PS Example: Fig 5 54pp; English.
CC The bivalent antigen-binding protein B72.3 Fv (R20184) is an example
CC of the antigen-binding proteins of the invention. They comprise a
CC first Fv fragment bound to at least one other Fv fragment by a
CC linker which keeps the Fv fragment apart. The connecting structure
CC of R20184 comprises a joining sequence derived from a human IgG1
CC domain linked to a complete human IgG4 hinge region. R20185 is the
CC sequence of the shortened hinge version of the B72.3 single chain Fv
CC hinge.
SQ Sequence 819 BP; 218 A; 198 C; 214 G; 189 T;

Query Match 39.4%; Score 294; DB 1; Length 819;
Best Local Similarity 66.3%; Pred. No. 7.5e-73;
Matches 439; Conservative 0; Mismatches 220; Indels 3; Gaps 1;

QY 4 GCGGATATCCAGATGACCCAGTCCCGTCCCTCTGTCGGCGATAGGTC 63
  |||
Db 64 GCGGATATCCAGATGACCCAGTCCCGTCCCTCTGTCGGCGATAGGTC 123
  |||
QY 64 ACCATCACTTCGCGCGCCAGCAAAACATCTATGGCGGCTGAACCTGGTATCAACGTAAA 123
  |||
Db 124 ACCATCACTTCGCGCGCCAGCAAAACATCTATGGCGGCTGAACCTGGTATCAACGTAAA 183
  |||
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QY 124 CTTGGGAAGCTCCGAGCTTCTGATTTACGTCGCGAAGCTGGCAGATGGATCCCT 183
 DB 184 CAGGAAATCTCTCCAGCTCTGCTATGCTGCACAACTTAGCAGATGGTGGCAG 243
 QY 184 TCTGCTTCTGATCGGCGGCGGAGCGATTCATCTGACATGACATGCTGGCAG 243
 DB 244 TCAAGTTCACTGGCAGTGAATCGGCGACACAGTATTCCTCAAGATCAACGCTGGCAG 303
 QY 244 CTTGAGACTTCGCTACATTTACTGTCAGAACGTTTAAATCTCCGTTGATTCGGA 303
 DB 304 TCTGAAATTTTGGGAGTATTACTGTCACATTTTGGGAGTACTCCGACACGTTTCGA 363
 QY 304 CAGGATCCAAAGTGGAAATAAACGTAAGTGGCGGTGTTCTGTTGGTGGCGTGAATCT 363
 DB 364 GGGGAGCAAGCTTGAATAAACG---TGGTGGCGGGGATCCGGGGGGAGGATTA 420
 QY 364 GTGTGTGGCGTTCTCAAGTCCCACTGGTGCATCCGGCGCGGAGTCAAGAACGAGG 423
 DB 421 GGGGATGGCGGATCCAGGTTCAAGTGCAGAGTGTGACGCTGAGATTTGGTAAACCTGGG 480
 QY 424 GCTCAGTCAAAAGTGTCTTAAGCTAGCGGCTATATTTTCTTAATTTATGATTCAA 483
 DB 481 GCTTCAATGAAGATATCTCGCAAGGCTTCTGCTACACCTTCACCTACATCTATTCAC 540
 QY 484 TGGGTGCGTCAAGGCCCCCGGCGAGGCTCGAATGATGGTGAATCTTACCGGCTCT 543
 DB 541 TGGGCGAAGCAGAGACCGGAGGCGCTGAGATGATTTGATATTTCTCCGGAAT 600
 QY 544 GTTAGCACCAGATATACCGAAATTTTAAAGACGCTGTACTANGACCGGTGACACTTCG 603
 DB 601 GATGATTTTAAATGACATGAGAAAGTTCAAGGCGCAAGCCACACTGATGACAGCAAAATCC 660
 QY 604 ACTAGTACAGATATACAGAGAGCTCTCCAGCTCGCATGGGAGAGACGCGCTCATATAT 663
 DB 661 TCCAGCACTGCTACATGACAGCTCAACAGCCTGACATCTGAGGATTTGCAAGTATTTTC 720
 QY 664 TG 665
 DB 721 TG 722
 RESULT 11
 ID 042284 standard; cDNA; 723 BP.
 AC 042284;
 DE 13-SEP-1993 (first entry)
 KW Type I ribosome-inactivating protein; ricin; gelonin;
 KW immunotoxin; autoimmunity disease; cell killing; toxin;
 KW overlap extension polymerase chain reaction; H65 variable region;
 KW RMA; rabbit muscle aldolase; cathepsin cleavage;
 KW SLT; E.coli Shiga-like toxin; human engineered antibody; ss.
 OS Synthetic.
 PN W09309130-A.
 PD 13-MAY-1993.
 PF 04-NOV-1992; U09487.
 PR 04-NOV-1991; US-787567.
 PR 19-JUN-1992; US-901707.
 PA (XOMA) XOMA CORP.
 PI Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
 DR WPI: 93-167617/20.
 PT Analogues of type I ribosome inactivating protein - useful as
 PT cytotoxic agents, immuno toxins for treating auto immune diseases,
 PT cancer, graft versus host disease and selective cell killing in-vivo
 PS Example 12; Page 123-124; 163pp; English.
 CC A single chain antibody form of the he3 H65 variable domain was
 CC assembled from previously constructed genes. This scab segment
 CC consisted of the entire V and J region of one chain (heavy or
 CC light) linked to the entire V and J segment of the other (light or
 CC heavy) via a 15 amino acid flexible peptide. The scab was assembled
 CC in two orientations (see 042284 and 042285). A fusion construct was
 CC prepared in which the natural sequence gelonin gene was positioned
 CC at the N-terminus and the SLT or RMA linker peptide was positioned

CC between the gelonin and scab domains.
 SQ Sequence 723 BP; 178 A; 162 C; 207 G; 176 T;
 Query Match 37.9%; Score 283.4; DB 1; Length 723;
 Best Local Similarity 63.7%; Pred. No. 6, 4e-70;
 Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;
 QY 7 GATATCAGATGACCCAGTCCCGTCTCCGCTTCGCGCTTGGGCGATAGGTCACC 66
 DB 1 GACATCAATGACATGATGCTCATCTTCCCTGTCATCTTAGAGACAGATCACT 60
 QY 67 ATCACCTGGCGGCCACGCAAAACATCTATGCGCCCTGACTGATCAACCTAACT 126
 DB 61 ATCACTTGGCGGCGAGTCAAGACATTAAATAGCTATTAAAGCTGTTCCAGGAACCA 120
 QY 127 GGGAAAGTCCGAAGCTTGTGATTTACGTTGCGACAGAACCTGGCAGATGAGTCCCTCT 186
 DB 121 GGGAAAGTCTTAAGACCTGATCTATCGTCAAAACAGATGGAATCTGGGGTCCCATCA 180
 QY 187 CGCTTCTGATCCGCGTCCGGAAGGANTTCACTCTGACATCAAGCATCTGCAAGCT 246
 DB 181 AGGTTAGTGAAGTGAATCTGGGACAGATTAATCTCAACATCAAGCAGCTGCAATAT 240
 QY 247 GAAGACTTGGTACGATTAATCTGCAAGACGTTTAAATCTCCGTTGACTTGGACAG 306
 DB 241 GAAGATTTTGGATTTATTTATTTGTCAACATATGATGATGATCTCCGTTGACGTTG 300
 QY 307 GGTACCAAGTGGAAATAAACGTAAGTGGCGGTGTTCTGTTGTTGCGGCTGATCTGT 366
 DB 301 GGCACCAAGCTGAGATGAAA-----GGTGGGGTGGATCTGTTGAGAGTGGGTCCGGA 354
 QY 367 GGTGGCGTTTCTCACTGATCCAGTGGTGCATCCGGCGCGAGGTCAAGAACGAGGCC 426
 DB 355 GGTGGAGATCTGAATCCAGTGGTGCATGGAGGAGGCGCTGTTGAGGCTGAGAGG 414
 QY 427 TCAGTCAAGTGTCTTAAGCTAGCGGCTATATTTTCTAATTTATGATTCATATG 486
 DB 415 TCCGTAGATCTCTGCGCAGCTTCTGGTATACCTTCAACATGATGAAATGAATGG 474
 QY 487 GTGCGTCAAGCCCCCGGCGAGGCTCGAATGATGGTGAATCTTACCGGCGCTGTGT 546
 DB 475 GTGCGCGAAGCTCCAGGAAGGTTAGAGTGAATGGCGGTGAATAACACCACTGGA 534
 QY 547 AGCACCAGATATACGAAATTTTAAAGACGCTGTACTATGACGCGGTGACACTTGACT 606
 DB 535 GAGCCACATATAGCTGATTTCTTCAAGGAGCGGTTTACCTTCTTGGACGATTTCAAG 594
 QY 607 AGTACGATATACATGAGGCTCTCCAGCTCGCATGGGAGACACGCGCTTATTTGTC 666
 DB 595 AACACTGCTATTTACAGATCAACAGCTTCAGAGCGGAGACAGGCTGTATTTCTGT 654
 QY 667 GCGCGTATTTTGTGTTCTAGCCCGAATTTGATTTGATTTGGTGGGTCAAGAAC 726
 DB 655 ACAAGAGCGGGTTAGC-----ACTGCTACTTGATGTCTGGGCGCAAGGAGAC 702
 QY 727 GTGTCACTGTCTCGAGCTGA 747
 DB 703 ACGGTCAACGCTCTCCATGA 723
 RESULT 12
 ID T94963 standard; DNA; 1065 BP.
 AC T94963;
 DE 20-APR-1998 (first entry)
 KW R. pipiens recombinant RNase ronc fusion protein 1 DNA.
 KW RNase A; ribonuclease; cytotoxic; onconase; none; immunofusion;
 OS Synthetic.
 PN W09731116-A2.
 PD 28-AUG-1997.

PF 19-FEB-1997; U02588.
 PR 21-FEB-1996; US-011800.
 PI (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Boque L, Newton DL, Rybak SM, Wlodawer A;
 DR WPI: 97-435168/40.
 DR P-PSDB; W35125.
 PT Ribonuclease molecules based on native Onconase - used for killing
 PT cells, particularly tumour cells
 PS Disclosure; Page 67; 90pp; English.
 CC Sequences T94963 to T94973 encode recombinant fusion proteins (rOnc)
 CC which are modifications of the RNase Onconase (RTM) (nOnc). Such novel
 CC ribonuclease molecules are highly cytotoxic and can be used alone or
 CC to form chemical conjugates or to target recombinant immunofusions. They
 CC are used particularly for decreasing tumour cell growth. They can also be
 CC used for cell separation in vitro by selectively killing unwanted types
 CC of cells, e.g. in bone marrow prior to transplantation into a patient
 CC undergoing marrow ablation by radiation, or for killing leukaemia cells
 CC or T-cells that would cause graft versus host disease. The toxins can
 CC also be used to selectively kill unwanted cells in culture. The new
 CC ribonucleases have increased cytotoxic activity compared to nOnc and also
 CC lower immunogenicity in humans. 240 C; 252 G; 272 T;
 SQ Sequence 1065 BP; 301 A; 240 C; 252 G; 272 T;

Query Match 35.7%; Score 267; DB 1; Length 1065;
 Best Local Similarity 63.4%; Pred. No. 2.7e-65;
 Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;
 QY 7 GATATCCAGATGACCCAGTCCCGTCCCTGTCGCCCTCTGTGGGCGATAGGTCACC 66
 DB 1 GACATCAAGATGACCCAGTCCCTGTCGCCCTCTGTGGGCGATAGGTCACC 60
 QY 67 ATCACTGCGGCGCCAGGAAACATCTATGCGCGCTGAAGTGTATCAAGTAAACCT 126
 DB 61 TTCATTGCAAGCGGATCAGGACATTAATCTATGTCGTTCCAGCAGAAACCA 120
 QY 127 GGGAAAGCTCCGAAGCTTCTGATTTACGGTGGGACGAACTGGCAGATGGAGTCCCTTCT 186
 DB 121 GGGAAATCTCCTTAAGACCTGATCTATCTGCAAAACAGACTGCTAGATGGGTCCTCATCA 180
 QY 187 CGCTTCTCTGATCCCGCTCCGGAACGATTTCACTCTGACCATCAGAGTCTGACGCT 246
 DB 181 AGGTTTCAGTGGCAGTGGATCTGGACAAAGATTTATCTCTACCATTAGCAGCTTGGAGTAT 240
 QY 247 GAAGATTCCTCGTACGATTTACTGTGACAAAGCTTTTAAATACCTCCGTTGACTTTTCGGACAG 306
 DB 241 GAAGATATGGGAATTTATTATTGTTCTACAGTATGATGAGTTTCCGTACAGCTTCGGAGGG 300
 QY 307 GGTACCAAGTGGAAATAAAAGCTACTGGCGGTGGTGGTCTGCTGGTCCGCGGTGGATCTGGT 366
 DB 301 GGGACCAAGCTGGAAATAAA-----GGAGGCGGTGGCTCGGCGGTGGCGGATCGGT 354
 QY 367 GGTGGCGGTCTCAAGTCCAACTGGTGCAATCCGGCGCGGAGTCAAGAGCCAGGGGCC 426
 DB 355 GCGGCGGCTCTGAGTTCAGCTCCAGCAGTCTGAGCTGCTACTTGGCAAGGCGCTGGGGCT 414
 QY 427 TCAGTCAAAGTGTCTCTGTAAGTCCAACTGGTGCATCCGGCGCGGAGGTCAAGAGCCAGGGGCC 486
 DB 415 TCAGTGAAGATGCTCTGCAAGGCTTCTGGCTACACCTTTTCCAGTACTGGATGACACTGG 474
 QY 487 GTGCGTCAAGGCTCCGCGGCGGCTGGAATGGATGGGTGAGATCTTACCAGGCTCTGGT 546
 DB 475 ATAAACAGAGGCTTGGACAGGCTTGGACCTGGAATGTCGCTATTGATCTCTGCAATAGT 534
 QY 547 AGCACCAATATCCGAAATTTTAAAGACCGGTGTACTATGACCGCTGACACTTCGACT 606
 DB 535 GATACTATTTACACCCCAATTTCAACACAAAGGCGCAAACTGACTGCTGAGTCACTCCACC 594
 QY 607 AGTACATATACATGGAGCTCTCCAGCTCGGATCGGATCGGAGGACAGCGGCTGTATTATGCG 666
 DB 595 AGCATGCTACATGGAACTCAACAGCCTGACAAATGAGGACTCTGCGGTCTATTACTGT 654
 QY 667 GCGGTTATTTTT 679

DB 655 ACCCTCTCTTATT 667
 RESULT 13
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 ID T94967 standard; DNA; 1065 BP.
 AC T94967;
 DT 20-APR-1998 (first entry)
 DE R. pipiens recombinant RNase rOnc fusion protein 5 DNA.
 KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
 KW tumour cell growth; frog; ss.
 OS Rana pipiens.
 OS Synthetic.
 PN W09731116-A2.
 PD 28-AUG-1997; U02588.
 PF 19-FEB-1997; U02588.
 PR 21-FEB-1996; US-011800.
 PI (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Boque L, Newton DL, Rybak SM, Wlodawer A;
 DR WPI: 97-435168/40.
 DR P-PSDB; W35129.
 PT Ribonuclease molecules based on native Onconase - used for killing
 PT cells, particularly tumour cells
 PS Disclosure; Page 71; 90pp; English.
 CC Sequences T94963 to T94973 encode recombinant fusion proteins (rOnc)
 CC which are modifications of the RNase Onconase (RTM) (nOnc). Such novel
 CC ribonuclease molecules are highly cytotoxic and can be used alone or
 CC to form chemical conjugates or to target recombinant immunofusions. They
 CC are used particularly for decreasing tumour cell growth. They can also be
 CC used for cell separation in vitro by selectively killing unwanted types
 CC of cells, e.g. in bone marrow prior to transplantation into a patient
 CC undergoing marrow ablation by radiation, or for killing leukaemia cells
 CC or T-cells that would cause graft versus host disease. The toxins can
 CC also be used to selectively kill unwanted cells in culture. The new
 CC ribonucleases have increased cytotoxic activity compared to nOnc and also
 CC lower immunogenicity in humans. 241 C; 250 G; 273 T;
 SQ Sequence 1065 BP; 301 A; 241 C; 250 G; 273 T;

Query Match 35.7%; Score 267; DB 1; Length 1065;
 Best Local Similarity 63.4%; Pred. No. 2.7e-65;
 Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;
 QY 7 GATATCCAGATGACCCAGTCCCGTCCCTGTCGCCCTCTGTGGGCGATAGGTCACC 66
 DB 1 GACATCAAGATGACCCAGTCCCTGTCGCCCTCTGTGGGCGATAGGTCACC 60
 QY 67 ATCACTGCGGCGCCAGGAAACATCTATGCGCGCTGAAGTGTATCAAGTAAACCT 126
 DB 61 TTCATTGCAAGCGGATCAGGACATTAATCTATGTCGTTCCAGCAGAAACCA 120
 QY 127 GGGAAAGCTCCGAAGCTTCTGATTTACGGTGGGACGAACTGGCAGATGGAGTCCCTTCT 186
 DB 121 GGGAAATCTCCTTAAGACCTGATCTATCTGCAAAACAGACTGCTAGATGGGTCCTCATCA 180
 QY 187 CGCTTCTCTGATCCCGCTCCGGAACGATTTCACTCTGACCATCAGAGTCTGACGCT 246
 DB 181 AGGTTTCAGTGGCAGTGGATCTGGACAAAGATTTATCTCTACCATTAGCAGCTTGGAGTAT 240
 QY 247 GAAGATTCCTCGTACGATTTACTGTGACAAAGCTTTTAAATACCTCCGTTGACTTTTCGGACAG 306
 DB 241 GAAGATATGGGAATTTATTATTGTTCTACAGTATGATGAGTTTCCGTACAGCTTCGGAGGG 300
 QY 307 GGTACCAAGTGGAAATAAAAGCTACTGGCGGTGGTGGTCTGCTGGTCCGCGGTGGATCTGGT 366
 DB 301 GGGACCAAGCTGGAAATAAA-----GGAGGCGGTGGCTCGGCGGTGGCGGATCGGT 354
 QY 367 GGTGGCGGTCTCAAGTCCAACTGGTGCAATCCGGCGCGGAGTCAAGAGCCAGGGGCC 426
 DB 355 GCGGCGGCTCTGAGTTCAGCTCCAGCAGTCTGAGCTGCTACTTGGCAAGGCGCTGGGGCT 414
 QY 427 TCAGTCAAAGTGTCTCTGTAAGTCCAAAGCTGTCAGCGCTATATTTTTTCTTAATTATTGGATCAATGG 486

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Db 415 TCAGGAAGATGCTCTGGAAGGCTTCTGGCTACACCTTTCCAGCTACTGATGACCTGG 474
QY 487 GTGGCTGAGCCCGGCGGAGGCTGTGAATGATGAGATCTTACCGGCTCTGGT 546
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QY 547 AGCACCAGATATACGAAATTTTAAAGACCGTGTACTATGACGGTGCACCTTGACT 606
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QY 607 AGTACAGATATACATGAGACTCTCCAGCTGCGATGAGAGAACGCGCTCTATTATTCG 666
Db 595 AGCACTGCTACATGGAAGACTCAACAGCCTGACCAATGAGGACTCTGCGGTCTATTACTGT 654
QY 667 GCGGCTTATTTT 679
Db 655 ACCCCTTTTATT 667

RESULT 14
ID T94965 standard; DNA; 1074 BP.
AC T94965;
DE 20-APR-1998 (first entry)
DE R. pipiens recombinant RNase ronc fusion protein 3 DNA.
KM RNase A; ribonuclease; cytotoxic; onconase; nonc; immunofusion;
KM tumour cell growth; frog; ss.
OS Rana pipiens.
OS Synthetic.
PN WO9731116-A2.
PD 28-AUG-1997.
PF 19-FEB-1997; U02588.
PR 21-FEB-1996; US-011800.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Bogue L, Newton DL, Rybak SM, Wlodawer A;
DR P-PSDB; W35127.
DR P-PSDB; W35127.
PT Ribonuclease molecules based on native Onconase - used for killing
PT cells, particularly tumour cells.
PS Disclosure; Page 69; 90pp; English.
CC Sequences T94963 to T94973 encode recombinant fusion proteins (rOnc)
CC which are modifications of the RNase Onconase (RTM) (nonc). Such novel
CC ribonuclease molecules are highly cytotoxic and can be used alone or
CC to form chemical conjugates or to target recombinant immunofusions. They
CC are used particularly for decreasing tumour cell growth. They can also be
CC used for cell separation in vitro by selectively killing unwanted types
CC of cells, e.g. in bone marrow prior to transplantation into a patient
CC undergoing marrow ablation by radiation, or for killing leukaemia cells
CC or T-cells that would cause graft versus host disease. The toxins can
CC also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nonc and also
CC lower immunogenicity in humans.
SQ Sequence 1074 BP; 304 A; 246 C; 250 G; 274 T;

Query Match 35.7%; Score 267; DB 1; Length 1074;
Best Local Similarity 63.4%; Pred. No. 2.7e-65;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

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Db 535 AGGTCAGTGGCAGTGGATCTGACAAAGATTATTCTCTACACCTTAGCACCTGGAGTAT 594
QY 247 GAAGACTTGCTGCTACGATTAATCTGACGAACGTTTAAATACCTCCGTTGATCGACAG 306
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QY 307 GGTACCAAGGTGGAATAAAGCTACTGGCGGTGTGTCTGTGTGTGTGTGTGTGTGTGTGT 366
Db 655 GGGACCAAGCTGGAATAA-----GGAGGGGGTGGCTGGGGCGGTGGCGGATGGGT 708
QY 367 GGTGGCGGTCTTCAGTCCAACTGTGCAATCCGGCGCGAGGTCAAGAACCGAGGGGCC 426
Db 709 GGGGGGGGCTCTGAGGTTGACCTCCAGCTGCGAGCTGGGACCTGTACTGGCAAGGCTGGGGCT 768
QY 427 TCAGTCAAGTGTCCCTTAAGCTACGGCTATATTTTCTATATTTGATGATTCATAGG 486
Db 769 TCAGTCAAGTGTCTGCAAGGCTTGTGCTACACCTTTTCCAGTCTGAGTACCTGG 828
QY 487 GTGCTGAGGCGCCCGGAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 546
Db 829 ATAAACAGAGGCGCTGACAGAGGCTGTGACCTGATGCTGCTATTGATCTCGAATACT 888
QY 547 AGCACCAGATATACGAAATTTTAAAGACCGTGTACTATGACGCGGTGACACTTGACT 606
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Db 1009 ACCCCTTTTATT 1021

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RESULT 15
ID T94968 standard; DNA; 1074 BP.
AC T94968;
DE 20-APR-1998 (first entry)
DE R. pipiens recombinant RNase ronc fusion protein 6 DNA.
KM RNase A; ribonuclease; cytotoxic; onconase; nonc; immunofusion;
KM tumour cell growth; frog; ss.
OS Rana pipiens.
OS Synthetic.
PN WO9731116-A2.
PD 28-AUG-1997.
PF 19-FEB-1997; U02588.
PR 21-FEB-1996; US-011800.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Bogue L, Newton DL, Rybak SM, Wlodawer A;
DR P-PSDB; W35130.
DR P-PSDB; W35130.
PT Ribonuclease molecules based on native Onconase - used for killing
PT cells, particularly tumour cells.
PS Disclosure; Page 72; 90pp; English.
CC Sequences T94963 to T94973 encode recombinant fusion proteins (rOnc)
CC which are modifications of the RNase Onconase (RTM) (nonc). Such novel
CC ribonuclease molecules are highly cytotoxic and can be used alone or
CC to form chemical conjugates or to target recombinant immunofusions. They
CC are used particularly for decreasing tumour cell growth. They can also be
CC used for cell separation in vitro by selectively killing unwanted types
CC of cells, e.g. in bone marrow prior to transplantation into a patient
CC undergoing marrow ablation by radiation, or for killing leukaemia cells
CC or T-cells that would cause graft versus host disease. The toxins can
CC also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nonc and also
CC lower immunogenicity in humans.
SQ Sequence 1074 BP; 304 A; 244 C; 252 G; 274 T;

Query Match 35.7%; Score 267; DB 1; Length 1074;

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Best Local Similarity 63.4%; Pred. No. 2.7e-65;				Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;			
Qy	7	GATATCCAGATGACCCAGTCCCGCTCCCTCCCTGTCCTGTCGGGGGATAGGGTCAACC	66				
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Db	415	TTCACTTCAAGGCGAGTCAGGACATTAATACTATTATGCTGGTCCAGCAGAAACCA	474				
Qy	127	GGGAAGCTCCGAAGCTTCTGATTACGGTGGCAGAACCTGGCAGATGAGTCCCTTCT	186				
Db	475	GGGAATCTCCTAAGACCTGATCTATCGTGCAACAGACTGGTAGTGGGTCCCATCA	534				
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Qy	247	GAAGACTTCGCTACGTATTACTGTGAGAACGTTTAAATACCTCCGTTGACTTTCGGACAG	306				
Db	595	GAAGATATGGGATTTATTATTTGCTACAGTATGATGATTTCCGTACAGTTCGGAGGG	654				
Qy	307	GGTACCAAGTGGAAATAAAGCTACTGGCGGTGGTGGTTCCTGGTGGCGGTGATCTGGT	366				
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Qy	367	GGTGGCGGTTCTCAAGTCCACTGGTGCNAATCCGGCGCGAGGTCAAGAAGCCAGGGCC	426				
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Qy	667	GGCGGTTATTTTT	679				
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Search completed: September 12, 2000, 21:01:09
Job time: 3578 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 19:20:03 ; Search time 56.72 Seconds
(without alignments)
1811.604 Million cell updates/sec

Title: US-08-487-283a-8

Perfect score: 747
Sequence: 1 ANGCGCGATATCCAGATGAC.....TGGTCACTGTCGACACTGA 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160 *

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgnl_7/ptodata/1/ina/5B.COMB.seq:*
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6: /cgnl_7/ptodata/1/ina/PCrus.COMB.seq:*
7: /cgnl_7/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	294	39.4	819	3	US-08-400-115-3
2	283.4	37.9	723	1	US-07-988-430-92
3	283.4	37.9	723	1	US-08-425-336-89
4	283.4	37.9	723	2	US-08-488-113B-89
5	283.4	37.9	723	2	US-08-477-484B-89
6	283.4	37.9	723	3	US-08-646-360-89
7	283.4	37.9	723	6	PCT-US92-09487-92
8	267	35.7	1065	5	US-08-875-811-40
9	267	35.7	1065	5	US-08-875-811-48
10	267	35.7	1074	5	US-08-875-811-44
11	267	35.7	1074	5	US-08-875-811-50
12	267	35.7	1086	5	US-08-875-811-46
13	267	35.7	1137	5	US-08-875-811-42
14	250	33.5	729	1	US-08-230-843-3
15	250	33.5	729	3	US-08-636-936-3
16	247.2	33.1	916	1	US-08-121-054C-29
17	236.6	31.7	733	4	US-08-926-789-17
18	236.6	31.7	733	4	US-08-926-789-15
19	234.4	31.4	721	3	US-08-224-591-15
20	234.4	31.4	721	4	US-08-926-789-15
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24	232.4	31.1	2178	6	PCT-US91-09133-25
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26	231	30.9	6727	4	US-08-891-848-2

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28	230.6	30.9	1299	4	US-08-891-848-6	Sequence 6, Appl
29	230.6	30.9	1320	3	US-08-125-462-3	Sequence 3, Appl
30	230.6	30.9	1320	4	US-08-891-848-3	Sequence 3, Appl
31	230.6	30.9	6799	4	US-08-125-462-5	Sequence 5, Appl
32	230.6	30.9	6799	4	US-08-891-848-5	Sequence 5, Appl
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34	224.4	30.0	732	1	US-08-636-936-1	Sequence 1, Appl
35	223.2	29.9	6127	4	US-08-887-352B-1	Sequence 1, Appl
36	221.8	29.7	720	1	US-08-061-092A-2	Sequence 2, Appl
37	220.6	29.5	7305	1	US-08-286-740-4	Sequence 4, Appl
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39	218	29.2	737	4	US-08-860-174A-1	Sequence 1, Appl
40	216.2	28.9	1460	5	US-08-392-338A-18	Sequence 18, Appl
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42	216.2	28.9	1460	5	US-09-166-093-18	Sequence 18, Appl
43	215.8	28.9	797	2	US-08-323-445A-3	Sequence 3, Appl
44	215.8	28.9	797	2	US-08-515-903A-3	Sequence 3, Appl
45	215.8	28.9	797	6	PCT-US95-12840-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-400-115-3
Sequence 3, Application US/08400115
Patent No. 5864019
GENERAL INFORMATION:
APPLICANT: KING, David John
APPLICANT: MOUNTAIN, Andrew
APPLICANT: OWENS, Raymond John
APPLICANT: YARRANTON, Geoffrey Thomas
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08400,115
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,136
FILING DATE: 27-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,193
FILING DATE: 17-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/00935
FILING DATE: 11-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9012995.8
FILING DATE: 11-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 040283/0106 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..816
US-08-400-115-3

Query Match 39.4%; Score 294; DB 3; Length 819;
Best Local Similarity 66.3%; Pred. No. 2.6e-84;
Matches 439; Conservative 0; Mismatches 220; Indels 3; Gaps 1;

QY 4 GCCGATATCCAGATGACCCAGTCCCGCTCCCTCCCTGTCGCGCTCTGCGGATAGGCTC 63
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DB 184 CAGGAAATCTCTCAGCTCTGCTGCTATGCTGCAAACTTAGCAGATGGTGTGCA 243
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DB 244 TCAAGTTTCACTGCGAGTGGATCGGACACAGATATCCCTCAAGATCAACAGCTGCAG 303
QY 244 CCTGAAGATTTGGTACGATTTACTGTCAGAACGTTTTAAATPACCTGCTGATTCGGA 303
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QY 304 CAGGATACCAAGTGGAAATTAACGTTACTGCGGTGCTGCTGCTGCGGCTGATCT 363
DB 364 GGGGGGACCAAGCTGAAATAAAGG---TGGTGGCGGGGATCCGGCGGGAGGTTCA 420
QY 364 GGTGGTGGCGGTTCTCAAGTCAACTGGTCAATCCGGCGGAGGTCAAGAAGCCAGGG 423
DB 421 GGGGTGGCGGATCCAGTTTCACTGTCAGCTGAGCAGTCTGACCTGAGTTGGTGAACCTGG 480
QY 424 GCCTCAGTCAAGTGTCTGTAAGCTAGCGCTATATTTTCTAATTTATTTGATTTCAA 483
DB 481 GCTTCAGTGAAGATATCTCGAAGCTTCTGCTACACCTTCACTGACCATGCTATTAC 540
QY 484 TGGTGGCTAGCGGCGGCGGAGGCTTGAATGGATGGTGGTGAATCTTACCGGCTCT 543
DB 541 TGGCGAGCAGCAGGCTTGAACAGGCGCTGGAATGGATTTGATATATTTCTCCCGAAAT 600
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DB 721 TG 722

RESULT 2
US-07-988-430-92
Sequence 92, Application US/07988430
Patent No. 5416202
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
Preparation and Use for Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-07-988-430-92

Query Match 37.9%; Score 283.4; DB 1; Length 723;
Best Local Similarity 63.7%; Pred. No. 5.8e-81;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

QY 7 GATATCCAGATGACCCAGTCCCGCTCTCCCTGTCGCGCTCTGTCGCGATAGGTCACC 66
DB 1 GATATCCAGATGACCTCAGTCTCCATCTTCCCTGTCGATCTAGGAGACAGTCACT 60
QY 67 ATCACTGCGGCGCCAGCGAAACATCTATGCGCGCTGAACTGGTATCAACGTAACCT 126
DB 61 ATCACTTGGCGGCGAGTCAGGACATTAATAGCTATTAACTGGTTCCAGCAGAACCA 120
QY 127 GGGAAAGCTCCGAGCTTCTGATTTAGGTCGCGACCACTGSCAGATGGAGTCCCTTCT 186
DB 121 GGGAAAGCTCCTAAGACCTCTGATCTATCGTCAACAGAGATTTGGAATCTGGGTCATCA 180
QY 187 CGCTTCTCTGGATCCCGCTCCGGAACGGATTTTCACTCTGACCATCAGCAGCTGCGACCT 246
DB 181 AGTTTCAGTGGCAGTGGATCTGGGACAGATTAATATCTCTACCATCAGCAGCTGCAATAT 240
QY 247 GAAGACTTCGCTACGTATTACTCTCAGAACGTTTTAAATACTCCGTTGACTTTTCGGACAG 306
DB 241 GAAGATTTTGGATTTTATTATTCTCAACAGTATGATGAGTCTCCGTGGAGCTTCGGTGA 300
QY 307 GGTACCAAGGTGGAATAAAGCTACTGCGCGTGGTGGTCTGTCGCGGTGATCTGGT 366
DB 301 GGCACCAAGCTTGGATGAAA-----GGTGGCGGTGGATCTGCTGGAGGTGGTCCGGA 354
QY 367 GGTGGCGGTCTCAAGTCCCAACTGGTGAATCGGCGCCGAGGTCAAGAGCCAGGGGCC 426

Db 355 GGTGGAGGATCTGAGATCCAGTTGGTCTGAGAGAGCCCTGGTGAACCTGGAGGG 414
Oy 427 TCAGTCAAGATGCTCTGTAAGAGCTAGCGGCTATATTTTCTAATTATGATTCATAG 486
Db 415 TCCGTAGGATCTCTCGGAGCTCTGGGATACCTTCACAACTATGATGAACTGG 474
Oy 487 GTCCGTCAGGCCCCGGGAGGCGCTGGAATGATGGGTGATCTTAACGGGCTGTGT 546
Db 475 GTCCGCGAGGCTCCAGGAAGGGTTAGAGTGATGGCTGATTAACACACCACTGGA 534
Oy 547 AGACCGGAATATCCGAAATTTTAAAGACCGCTTACTATGAGCGCGAATCTGACT 606
Db 535 GACCCACATATGCTGATCTCTTCAAGGAGCGGTTACCTTCTTGGAGAGTTCTAG 594
Oy 607 AGTACAGTATACATGAGCTCTCCAGCTCGATCGAGACGAGCGGCTATATTGCG 666
Db 595 AACACGCGCTATTATTCAGATCAGACAGCTCAGACCGAGGACGCGTGTATTTCTGT 654
Oy 667 GCGCGTATTTTGTGTTCTAGCCGAATGATTTTGTGATTTGTTGGGTCAGGAACC 726
Db 655 ACAAGACGGGGTTACG-----ACTGGTACTTCGATGTCTGGGCGCAAGGAGAC 702
Oy 727 CTGCTACTCTCTCGAGCTGA 747
Db 703 ACGGTACCGCTCTCTCATGA 723

RESULT 3
US-08-425-336-89
Sequence 89, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-425-336-89

Query Match 37.9%; Score 283.4; DB 1; Length 723;
Best Local Similarity 63.7%; Pred. No. 5,8e-81;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

Oy 7 GATATCAGATGACCAGTCCCGCTCCCTCCCTGTCGCGCTCTGTGGCGATAGGTCACC 66
Db 1 GACATCCAGATGACTACGCTCCATCTTCCCTGTCTGATCTGTAGAGACAGAGTCACT 60
Oy 67 ATCACTGCGGCGCCAGGAAACATCTATGGCGCGCTGAACTGATTAACATTAACCT 126
Db 61 ATCACTTCCCGGCGAGTCAGACATTAATACCTTTTAAAGTGGTTCCAGCAAAACCA 120
Oy 127 GGAAGAGTCCGAGACTTCTGATTTACGGTGGAGGAACCTGGCAGATGGAGTCCCTCT 186
Db 121 GGAAGAGTCCCTAAGACCTGATCTATCTGTCGAAACAGATTGGAATCTGGGTCATCA 180
Oy 187 CGCTCTCTGATCCGCTCCGGAAGGATTTCACTCTGACCATCAGCATGCTGAGCCT 246
Db 181 AGGTTCAGTGGCAGTGAATCTGGGACAGATTTATCTCTCACCATCAGCAGCCTGCAATAT 240
Oy 247 GAAGACTTCGCTACTATTACTGTGAGAACGTTTAAATACTCCGTTGACCTTCCGACAG 306
Db 241 GAAGATTTTGGAAATTAATATTTGTCACAGATGATGATGATGATCCGTCGACGTTCCGTGA 300
Oy 307 GSTACCAAGTGGGAATTAACGCTACTGGCGGTGGTGGTCTGGTGGCGGTGGATCTGT 366
Db 301 GGCACCAAGCTTGAGATGA-----GGTGGCGGTGATCTGGTGGAGTGGGTCGGA 354
Oy 367 GTGGCGGTTTCAAGTCCAACTGTCGCAATCCGCGCGAGTCAAGAACGACGAGGCC 426
Db 355 GGTGGAGATCTGAGATCCAGTGTGTCAGTGTGAGAGGCGCTGTGAAGCTTGAGAGG 414
Oy 427 TCAGTCAAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTAATGATTCATAG 486
Db 415 TCCGTCAAAATCTCCTGGCAGCTTCTGGGTATACCTTCACAACTATGATGAATCTGG 474
Oy 487 GTGGTCAAGGCCCCGGGAGCGGCTGGAATGAGGCTGGAATCTTACCGGCTCTGT 546
Db 475 GTGGCGCAGGCTCCAGGAAGGGTTAAGTGAAGGCTGTGATAACACCCCACTGGA 534
Oy 547 AGACCGGAATATCCGAAATTTTAAAGACCGTGTACTATGACCGTGAACCTTCGACT 606
Db 535 GAGCCACATATGCTGATCTTTTCAAGGAGCGGTTTACTTCTCTTTGGACATTCITAG 594
Oy 607 AGTACAGTATACATGAGCTCTCCAGCTCGATCGAGACGAGACGCGCTCTATTATTGCG 666
Db 595 AACACTGCTATTATACAGATCAAGTCAAGCCTCAGAGCGAGACGCGGTGTATTCTGT 654
Oy 667 GCGCGTATTTTGTGTTCTAGCCGAATGATTTTGTGATTTGTTGGGTCAGGAACC 726
Db 655 ACAAGACGGGGTTACG-----ACTGGTACTTCGATGTCTGGGCGCAAGGAGAC 702
Oy 727 CTGCTACTCTCTCGAGCTGA 747
Db 703 ACGGTACCGCTCTCTCATGA 723

RESULT 4
US-08-488-113B-89
Sequence 89, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,113B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 110222US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 89:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 723 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-488-113B-89

Query Match 37.98; Score 283.4; DB 2; Length 723;
Best Local Similarity 63.78; Pred. No. 5.8e-81;
Matches 472; Conservative 0; Mismatches 18; Gaps 2;
QY 7 GATATCCAGATGACCCAGTCCCGCTCCCTGCTCCGCTCTGTGGCGATAGGCTCACC 66
Db 1 GACATCCAGATGACCTGCTCCATCTCCCTGCTGCTGATCTGTAGGAGACAGATCCT 60
QY 67 ATCACTCGCGGCGGAGCAAAACATCTATGCGCGCTGAACTGGTATCAACGTAACCT 126
Db 61 ATCACTTCCGCGGCGAGTCAGGACATTAATAGCTATTTAAGCTGTTCCAGCAGAACCA 120
QY 127 GGAAGAGCTCGAAGCTTCTGATTTACGGTGGGAGAACCTGGCAGATGGAGTCCCTTCT 186
Db 121 GGAAGAGCTCTAAGACCCCTGATCTATCTGCAAAACAGATTGGAATCTGGGCTCCCATCA 180
QY 187 CGCTTCTCGATCGGCTCGGAGCGGATTTCACTCTGACCATCAGCAGTCTGAGCCT 246
Db 181 AGGTTTCAGTGGCAGTGGATCTGGGACAGATTATCTCTCACCATCAGGCGCTGCAATAT 240
QY 247 GAAGACTTCGCTAGCTATTTACTGTGACAAACGTTTTAAATATCTCCGTTGACTTCCGACAG 306
||||| ||| | ||||| ||||| | | ||||| ||||| |||||

Db 241 GAAGATTTTGAATTTATTTATTTCAACAGATGATGATCTCCGTGGAGCTTCGGTGA 300
QY 307 GGTACCAAGGTGGAATAAAGCTACTGCGGTGCTGCTGCTGGTGGCGGTGATCTGCT 366
Db 301 GGCACCAAGCTTGAGATGAAA-----GGTGGCGGTGATCTGGTGGAGGTGGTCCGGA 354
QY 367 GGTGGCGGTCTCTAAGTCCAACTCCGCGCCGCGAGGTCAAGAAGCCAGGGGCC 426
Db 355 GGTGGAGGATCTGAGATCCAGTTGCTGAGTCTGGAGGAGGCTGTTGAAGCTTGAAGG 414
QY 427 TCAGTCAAGTGTCTCTGTAAGCTAGCGGCTATATTTTCTTAATATTGGAATCAATGG 486
Db 415 TCCGTCAGAAATCTCTGCGCAGCTTCTGGTATACCTTCACAAACTATGGAATGAATGG 474
QY 487 GTGCTGTCAGGCGCGCGGCGGCTGGAATGATGGTGGTGGATCTTACCGGGCTCTGCT 546
Db 475 GTGCGCCAGGCTCCAGGAAAGGTTTAGATGGTGGCTGGATTAACACCCACACTGA 534
QY 547 AGCACCGAATATACCGAAATTTTAAAGACCTGTTACTATGACGCGTGACACTTCGACT 606
Db 535 GAGCCAAACATATGCTGATCTTTCAAGGAGCGGTTTACCTTCTTGGACGATTTAAG 594
QY 607 AGTACAGTATACATGAGCTCTCCAGCCTGCGATCGGAGGACACGCGCTCTATTATTC 666
Db 595 AACACTGCTATTACAGATCAACAGCCTCAGAGCGGAGGACACGCGCTGTGATTTCTGT 654
QY 667 GCGGCTTATTTTGGTCTAGCCCGGATTTGGTATTTTGGTGGTCAAGGAACC 726
Db 655 ACAAGACGGGTTACG-----ACTGGTACTTCGATGTCTGGGGCCCAAGGGACC 702
QY 727 CTGGTCACTGCTCTCGAGCTGA 747
Db 703 ACGGTCACCGTCTCCTCATGA 723
RESULT 5
US-08-477-484B-89
; Sequence 89, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707

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1 FILING DATE: 19-JUN-1992
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: US 07/787,567
4 FILING DATE: 04-NOV-1991
5 ATTORNEY/AGENT INFORMATION:
6 NAME: McNicholas, Janet M.
7 REGISTRATION NUMBER: 32,918
8 REFERENCE/DOCKET NUMBER: 110220US07/200-70.P3.C2A
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: 312/707-8889
11 TELEFAX: 312/707-9155
12 TELEX: 650 388-1248
13 INFORMATION FOR SEQ ID NO: 89:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 723 base pairs
16 TYPE: nucleic acid
17 STRANDEDNESS: single
18 TOPOLOGY: linear
19 MOLECULE TYPE: DNA
20 JS-08-477-484B-89

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Query Match	37.9%	Score 283.4	DB 2	Length 723
Best Local Similarity	63.7%	Pred. No. 5.8e-81		
Matches 472; Conservative	0	Mismatches 251	Indels 18	Gaps 2

QY	7	GATATCCGAGTACGACCACTCCCGCTCCCTCCCTGTCGCGGCTCTGGGGCGAGTANGGCTACC	66
Db	1	GACATCCGAGTACCACTCACTCCACTCTCCCTGCTCTGATCTGTAGGACAGAGTCACT	60
QY	67	ATCACCTGGCGGCCGACAGGAAACAATCTATGCGCGCTGACACTGGTATCAACGTAAACCT	128
Db	61	ATTCACCTTGC CGGGGAGACAGACACATTAATTAAGCTATTAACCTGGTTCACAGCAACAACA	120
QY	127	GGGAAAGCTCCGAGACCTTCTGATTACGGTGCAGACGAACCTGGCAGATGGAGTCCCTTCT	188
Db	121	GGGAAAGCTCCTAAGAACCTTATCTATGCTGCACAAACGATTGGAAATCTGGGCTCCATCA	180
QY	187	CGCTTCTCTGGATCCGCGCTCCGGAACGGATTCACTCTGACCAATCAGCACTGTCAGCCT	248
Db	181	AGGTTCACTGTCAGTGGATCTGGGACAGATATATCTCTCACCAATCAGCAGCCTCAATAT	240
QY	247	GAAGACTCCGTAGTATTAATCTAGTCAGACCTTTAAATACCTCGGTAGCTATCTGGACAG	306
Db	241	GAAAGTTTTTGGAAATTTATTTATTTGTCACACAGTATGATGAGTCTCCGTGACCTTGGTGA	300
QY	307	GGTACCAAGAGTGGAATTAACAGTACTGCGCGGTGGTGTCTGGTGGCGGTGATCTGCT	366
Db	301	GGCAACAAGCTTGAGATGAATGAA-----GGTGGCGGTGATCTGGTGGAGGTGGGTCCGGA	354
QY	367	GGTGGCGGTTTCAAGTCCAACTGGTGCATTCGGGCGCCGACAGTCAAGAAAGCCAGGGGCC	426
Db	355	GGTGGAGGATCTGGAGATCCCACTTGGTGCACAGTCTGGAGAGGCCCTGGTGAAGCCCTGGAGGG	414
QY	427	TCAGTCAAAAGTGTACTGTAAGCTAGCGGCTATATTTTCTTAATTTATTTGATTCATG	488
Db	415	TCCGTCAAAATCTCTCGCGCAGCTTCTGGGTATATACCTTCAACAACTGATGAATAACTGG	474
QY	487	GTCGCTCAGGCCCCCGGGCAGGGCCTGGAAATGATGGGTAGATCTTACCGGGCTCTGGT	548
Db	475	GTCGGCCAGGCTCCAGGAAAGGGTTTAGAGTGGCTGGATTAACACCACCACTACGGA	534
QY	547	AGCAACCGAATATACCGAAATTTTAAAGACCGGTCTACTATGACGGCTGACACTTCGACT	606
Db	535	GAGCCACAAATGCTGATCTTTCATAGGACGCTTACCTCTCTTTGGACGATTTCTAAG	594
QY	607	AGTACAGTATACATGAGACTCTCCAGCCTGGCATCGAGACAGCGCGCTATATATTCG	666
Db	595	AACACTGCTATTTACAGATCAACAGCCTCAGAGCCGAGACAGCGCTGTGTATTTCTGT	654
QY	667	GGCGGTTATTTTTTGGTCTACGCCCAATTGGTATTTGATGTTTGGGGTCAAGAAC	728
Db	655	ACAAGACGGGGTTACG-----ACGTGACTTCGATGTGCTGGGGCAAGGGAC	702

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OY      727 CTGGTCACTGTCTCGAGCTGA 747
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Db      703 ACGGTACCGTCTCCTCATGA 723

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RESULT 6
US-08-646-360-89

; Sequence 89, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:

1
 2 APPLICANT: Better, Marc D.
 3 APPLICANT: Carroll, Stephen F.
 4 APPLICANT: Studzinska, Gary M.
 5
 6 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 7
 8
 9 TITLE OF INVENTION: Proteins
 10
 11
 12 NUMBER OF SEQUENCES: 173
 13
 14
 15 CORRESPONDENCE ADDRESS:
 16
 17

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530

APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/084,093
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430

; FILING DATE: 09-DEC-1992
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ;

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ;

NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.F
TELECOMMUNICATION INFORMATION.

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR CIO NO. 80.

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 723 base pairs
; TYPE: nucleic acid
; STRATEGY: sequencing

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;      TOPOLOGY:  linear
;      MOLECULE TYPE:  DNA
US-08-646-360-89

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	Score	DB	Length
Query Match	283.4	3	723
Best Local Similarity	5.8e-81		
Matches 472, Conservative	0		
			Indels 18; Gaps 2

QY 7 GATATCCAGATGACCCAGTCCCCTCCTCGCTGTCCGGCTCTGTGGGCATAGGGTCACC 66
 || ||||||| ||||| || ||||||| || ||||||| || ||||||| || |||||||
Db 1 GACATCCAGATGACTCAGTCTCCATCTTCCCTGTCGTGATCTGTAGGAGACAGAGTCACT 60

Db 535 GAGCAACATATGCTGATCTTTCAAGGAGCGTTACCTTCTTTGGACATTTCTAAG 594
QY 607 AGTACAGTATACATGAGAGCTCTCCAGCCTGCAGTGGAGAGACGCGCTATTATTTC 666
Db 595 AACACTGCTATTACATGATCAACAGCCTCAAGCGGAGACAGCGCTGTATTTCGT 654
QY 667 GCGGCTATTATTTTGGTTCTAGCCGAATTGGTATTGATGTTGGGGTCAAGAAC 726
Db 655 ACAAGAGCGGGGTACG-----ACTGTACTTCGATGCTGGGCGCAAGGAGAC 702
QY 727 CTGCTACTGCTCGAGCTGA 747
Db 703 ACGGTACCGCTCTCTCATGA 723

RESULT 8
US-08-875-811-40
Sequence 40, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1065
OTHER INFORMATION: /note="sfvBmetGlunc"
US-08-875-811-40

Query Match 35.7%; Score 267; DB 5; Length 1065;
Best Local Similarity 63.4%; Pred. No. 1.2e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 7 GATATCCAGATGACCCAGCTCCCGCTCCCTGTCGCGCTGTGGCGATAGGTCACC 66
Db 1 GATATCAAGATGACCCAGCTCCCATCTTCATGTATGATCATAGAGAGAGATCACT 60
QY 67 ATCACTGGGGGCCCGCAAGAAACATCTATGGGGCCCTGAACGTGATCAAGCTAACCT 126
Db 61 TTCACCTTGGAGCGGAGTCAAGACATTAATTAATTAATTAATTAATTAATTAATTA 120
QY 127 GGGAAAGCTCCGAAGCTTGTATGATGAGGAGACAGACACTGAGATGAGACCTTCT 186
Db 121 GGGAAATCTCTTAAGACCTGATCTTCTGCAAAAGACTGATGATGGGGTCCCATCA 180
QY 187 CGCTCTCTGATCCGCTCCGAGAGATTCCTGACATCAATCAAGTCAAGTCAAGCT 246
Db 181 AGGTTCAGTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 247 GAAGACTTGGCTAGTATTACTGTCAAGAGTTTAAATTAATTAATTAATTAATTAAT 306
Db 241 GAAGATATGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
QY 307 GGTACCAAGTGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 366
Db 301 GGTACCAAGTGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 354
QY 367 GGTGGGCTTCTCAAGTCCAGTGTCAATCCGCGCGCGAGTCAAGAGCCAGGAGGC 426
Db 355 GGTGGGCTTCTCAAGTGTCAATCCGCGCGCGAGTCAAGAGCCAGGAGGC 414
QY 427 TCAGTCAAGTGTCTGTAAGCTAGCGGCTATATTTTCTAATTAATTAATTAATTAAT 486
Db 415 TCAGTCAAGTGTCTGTAAGCTAGCGGCTATATTTTCTAATTAATTAATTAATTAAT 474
QY 487 GTCCGTACAGCCCGCGGAGAGGCTGGAATGATGATGATGATGATGATGATGATGAT 546
Db 475 ATAAACAGAGGCTGGAAGGCTGGAATGATGATGATGATGATGATGATGATGATGAT 534
QY 547 AGCAGCAATATACCAAAATTTAAAGACCGGTACTAGACGGGTGACACTTGACT 606
Db 535 GATCACTATTACACCCGCAATTCACACAGCCAACTGACTGACTGACTGACTGACT 594
QY 607 AGTACAGTATACATGAGGCTCTCCAGCTGCGATCGGAGAGACAGCGCGCTATTATT 666
Db 595 AGCACTGCTACATGAGACTCAACAGCCTGACAAATGAGAGACTCTCGGCTATTACT 654
QY 667 GCGGCTATTATTTT 679
Db 655 ACCCTCTTATT 667

RESULT 9
US-08-875-811-48
Sequence 48, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:


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Db 415 TTCACCTTCAGAGCGAGTCAGACATTAATACTATTATGCTGCTTCAGCAGAAACA 474
QY 127 GGAAGAGCTCCGACTTCTGATTTACGCTGCGAGCAACCTGCAGATGAGTCCCTTCT 186
Db 475 GGGAAATCTCCTAAGACCTGATCTATGCTGCAAAACAGCTGTAGATGGGTCCTATCA 534
QY 187 CGCTTCTGATCCGCTCCGGAACGATTTCACTGTGACATCAGAGTGTGACGCT 246
Db 535 AGGTTCAGTGGCAGTGAATCTGCAACAGATTAATTCCTCACCATTGACAGCCTGGAGTAT 594
QY 247 GAAGCTTCGCTACATTTACTGTAGAACGTTTAAATACCTCCGTTGACTTTCGACAG 306
Db 595 GAAGTATGGAATTTATTTATGTTACAGTATGATGAGTTCCTCCGACGCTCGAGAGG 654
QY 307 GGTACCAAGTGGGAATTAACGCTAGTGGCGGTGGTGTGTTGTTGGTGGGTGGATCTGCT 366
Db 655 GGGACCAAGCTGGAAATTAATA-----GGAGCGGTGGTCTCGGGCGGTGGCGATCGGCT 708
QY 367 GGTGGCGGTCTCAAGTCCCACTGCTGCAATCCGGCGCCGAGGTCAAGAACCGAGGGCC 426
Db 709 GCGCGCGCTCTGAGTTCAGCTCAGCTCAGCAAGTCTGGGACTGTACTGGCAAGGCTGGGGCT 768
QY 427 TCAGTCAAGAGTCTCTGTAACCTAGCGGCTATATTTTCTTAATTATTGATTCATGG 486
Db 769 TCAGTGAAGATGCTCTGCAAGGCTCTGCTACACCTTTTCCAGCTACTGATGACACTGG 828
QY 487 GTGGCTGAGCGCCCGGGGAGGGGCTGGAATGGATGGGTGATCTTACCGGCTCTGCT 546
Db 829 ATAAACAGAGGCTGGAGGGGTGTGAGTGTGATGCTGCTATGATCTCGAAATATG 888
QY 547 AGCAACCGAATATACCGAAATTTTAAAGCCGTGTACTATGACGGGTGACACTTGCAT 606
Db 889 GATCTATTATTAACCCCGAATTTCAACACAGGCCAATGACTGACATCTACCTCACC 948
QY 607 AGTACATATACAGTGAAGCTCTCCAGCCTGCGATCGAGAGACAGGCGCTCTATTATTC 666
Db 949 AGCACTGCCATGAGTGAAGTCAACAGCCTGACAAATGAGAGACTCTCGCTATTACTGT 1008
QY 667 GCGGCTTATTTT 679
Db 1009 ACCCTCTTATTT 1021

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RESULT 11
US-08-875-811-50
: Sequence 50, Application US/08875811
: Patent No. 6045793
: GENERAL INFORMATION:
: APPLICANT: Rybak, Susanna M.
: APPLICANT: Newton, Dianne L.
: APPLICANT: Boque, Luis
: APPLICANT: Wlodawer, Alexander
: TITLE OF INVENTION: Recombinant Ribonuclease Proteins
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/875,811
: FILING DATE: 19-FEB-1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US97/02588

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: FILING DATE: 19-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/011,800
: FILING DATE: 21-FEB-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Faris, Susan K.
: REGISTRATION NUMBER: 41,739
: REFERENCE/DOCKET NUMBER: 015280-244100US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1074 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1074
: OTHER INFORMATION: /note="MetJuncFBE6"
US-08-875-811-50

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Query Match 35.7%; Score 267; DB 5; Length 1074;

Best Local Similarity 63.4%; Pred. No. 1.2e-75; Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

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QY 7 GATATCCAGATGACCCAGTCCCGTCCCTCCGCTCTGTGGCGGATAGGATCACC 66
Db 355 GATACATAGATGACCCAGTCCCGTCCCTCCGCTCTGTGGCGGATAGGATCACC 414
QY 67 ATACCTCGGCGCCAGCGAAACATCTATGGCGCGCTGACCTGATCTCAAGTAACT 126
Db 415 TTCACCTGCAAGCGAGTCAAGCAATTAATATATGCTGCTCCAGCAAGAAACA 474
QY 127 GGAAGAGCTCCGAAGTGTGATTTACGGTGGAGCAGCACTGGAGATGAGTCCCTCT 186
Db 475 GGGAAATCTCTTAAGACCTGATCTATCTGCAAAACAGACTGTAGTGGGTCCATCA 534
QY 187 CGCTCTCTGATCCGCTCCGGAACGATTTCACTGTGACATCAAGCACTGACGCT 246
Db 535 AGGTTCAGTGGCAGTGTGATGCAAGATTTATCTCTCACCATTAGCAACCTCGAGTAT 594
QY 247 GAAGACTTGGCTACGTTACTGTCAAGACGTTTAAATATCCGTTGACTTTCGACAG 306
Db 595 GAAGATATGGGAATTTATTTGTTCAAGTATGATGATGATTCGCTACAGCTTCGAGG 654
QY 307 GGTACCAAGTGGAAATTAACGATCTAGGGGTGGTGTCTGTGGCGGTGATCTGCT 366
Db 655 GGGACCAAGCTGGAAATTAATA-----GGAGGGGTGGTCTCGGGCGGTGGCGATCGGCT 708
QY 367 GGTGGCGGTCTCAAGTCCCACTGCTGCAATCCGGCGCCGAGGTCAAGAACGAGGGCC 426
Db 709 GCGCGGCTCTGAGTTCAAGTTCAGCTCAGCACTGTGGGACTATGTGCAAGGCTCGGGCT 768
QY 427 TCAGTCAAGAGTCTCTGTAAGCTAGCGGCTATATTTTCTAATATTGATTCATGAG 486
Db 769 TCAGTGAAGATGCTGCAAGGCTTGTGCTACACCTTTCCAGCTACTGATGACACTGG 828
QY 487 GTGCGTCAAGCGCCCGGGGAGGCGCTGGAATGGATGGGTGAGATCTTACCGGCTCTGCT 546
Db 829 ATAAACAGAGCGCTGAGAGGGGTCTGAGTGTGCTGCTATGATCTCGAAATATG 888
QY 547 AGACCGAATATACCGAAATTTTAAAGACCGTTACTATGACGCGCTGACCTGACAT 606
Db 889 GATACATTTTCAACCCCGAATTTCAACACAGGCCAAGCAAGTCAAGTCAAGTCAAGTCA 948
QY 607 AGTACATATACATGAGCTCTCAGCTCAGCTGATGGAGACAGGCGCTATATTATTC 666
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QY 667 GCGGTTATTTT 679
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Db 1009 ACCCTCTTTATT 1021

RESULT 12
US-08-875-811-46
; Sequence 46, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1083
; OTHER INFORMATION: /note= "MetSerOnCangSv"
US-08-875-811-46

Query Match 35.7%; Score 267; DB 5; Length 1086;
Best Local Similarity 63.4%; Pred. No. 1.2e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 7 GATATCCAGATGACCCAGTCCCGCTCTCCCTGTCGCGCTCTGTGGCGGATAGGGTCACC 66
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Db 361 GACATCAAGATGACCCAGTCTCCATCTTCCATGTATGTCATCTCTAGAGAGAGATCACT 420
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Db 421 TTCACCTGCAAGCGAGTCAGGACATTAATACTATTATGCTGGTTCACGACAGAACCA 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 GGGAAAGCTCCGAACTTCTGATTACGGTGGCGACCAACTGGCAGATGGATCCCTTCT 186
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481 GGGAAATCTCTAAGACCCCTGATCTATCGTCAACACAGACTGCTAGATGGGTCCTCATCA 540
187 CGCTTCTCTGGATCCGCTCCGGAACGGATTTCACCTCTGACCATCAGACTCTGACGCT 246
541 AGGTCAGTGGCAGTGGATCTGGCAAGAATATTCTCTACCAATTAGCAGCTTGGAGTAT 600
247 GAAGACTTCGCTACGTATTACTCTCAGAACGTTTTAAATACTCCGTTGACTTTCCGGACAG 306
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601 GAAGATATGGAAATTTATTATTCTCTACAGTATGATGAGTTTCCGTACACGTTCCGGAGGG 660
307 GGTACCAAGGTGAAATATAACCTACTGGCGGTGGTGGTTCCTGGTGGCGGTGATCTGGT 366
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661 GGGACCAAGCTGGAATAAAAA-----GGAGCGGCTGGCTCGGCGGTGGCGGATCCGGT 714
367 GGTGGCGGTTCTCAAGTCCCAACTGGTGCAATCCGCGCGCGAGGTCAAGAAGCCAGGGGCC 426
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715 GCGCGCGGCTCTGAGGTTCAGCTCCAGACTCTGGGACTTACTGGCAAGGCTTGGGGCT 774
427 TCAGTCAAAGTGTCTGTTAAAGCTAGCGGCTATATATTTTCTAATTATTGGATTCAATGG 486
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
775 TCAGTGAAGATGCTCTCAAGGCTTCTGGCTACACCTTTTCCAGCTACTGGATGCACTGG 834
487 GTCCGTGAGGCCCGCGCGGCGAGGCTTGAATGGATGGGTGAGATCTTACCGGGCTCTGGT 546
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
835 ATAAACACAGAGGCTTGACAGGCTCTGGACTGGATGTTGCTGCTATTCGCTTATTCGAAATAGT 894
547 AGCACCAGATATACCGAAATTTTAAAGACCGTGTACTATGACGCTGACGCTTATTCGACT 606
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895 GATACTATTTCACACCGCAATTCACACACAGGCAAACTGACTGCAGTCACTCCACC 954
607 AGTACAGATATACATGGAGCTCTCCAGCTCGGATCGGAGGACACGCGCTCTATTATTTC 666
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955 AGCACTGCCTACATGGAATCAACAGGCTGACAGGCTGACAAATGAGGACTTGGGCTTATTCTGT 1014
667 GCGCGTTATTTT 679
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Db 1015 ACCCTCTTTATT 1027

RESULT 13
US-08-875-811-42
; Sequence 42, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1083
; OTHER INFORMATION: /note= "MetSerOnCangSv"
US-08-875-811-46

Query Match 35.7%; Score 267; DB 5; Length 1086;
Best Local Similarity 63.4%; Pred. No. 1.2e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 7 GATATCCAGATGACCCAGTCCCGCTCTCCCTGTCGCGCTCTGTGGCGGATAGGGTCACC 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GACATCAAGATGACCCAGTCTCCATCTTCCATGTATGTCATCTCTAGAGAGAGATCACT 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 67 ATCACTGCGGCGCAGCGAAACATCTATGGCGCCCTGAATGGTATCAACCTAACT 126
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Db 421 TTCACCTGCAAGCGAGTCAGGACATTAATACTATTATGCTGGTTCACGACAGAACCA 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 GGGAAAGCTCCGAACTTCTGATTACGGTGGCGACCAACTGGCAGATGGATCCCTTCT 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

? NAME: Faris, Susan K.
? REGISTRATION NUMBER: 41.739
? REFERENCE/DOCKET NUMBER: 015280-244100US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 42:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1137 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1137
? OTHER INFORMATION: /note="SignalonCDBE6
US-08-875-811-42

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Query Match	35.7%	Score	267	DB	5	Length	1137
Best Local Similarity	63.4%	Pred. No.	1.2e-75				
Matches	427	Conservative	0	Mismatches	240	Indels	6
						Gaps	1

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QY	67	ATCACCTGCGGCGCCAGCCGAAACATCTATGGCGCGCTGAATGGTATCAACGTAAACCT	126
Db	487	TTCACTTCAAGGCGAGTACGAGCATTAATTAATTAATTTATGGTGGTTCAGGACAAACCA	546
QY	127	GGGAAAGCTCCGAAGCTTCTTGATTTACGGTGGCAGCAACCTGGCAGATGAGTCCCTTCT	186
Db	547	GGGAAATCTCCTAAAGACCTCGATCTATCGGCAACAGACTGGTATGATGGGTCCCATCA	606
QY	187	CGCTTCTCTGGATCCGCGCTCCGGAGAGGATTCACCTCAGCATACAGTGTGACGCT	246
Db	607	AGGTTCACTGGCAGTGGATGTGGACAAGATTAATTCCTTCCATTAAGCCCTGGAGAT	666
QY	247	GAAAGCTTCGCTACGTATTAATCTCAGAAAGTTTAAATCACTCCGTGACTTTCGGATAG	306
Db	667	GAAATATATGGGAATTTATTTATGTCTACAGTATGATGAGATTCCGTACACGTTCCGAGG	726
QY	307	GGTACCAAGGTGGAAATAAACGTACTGGCGGTGATGTCTGTGTGGCGGTGATCTGT	366
Db	727	GGGACCAAGCTGGAAATAAAA-----GGAGCGGTGGCTCGGGCGGTGGCGGATCGG	780
QY	367	GGTGGCGGTTCTCAAGTCCAACTGGTGGCAATCCGGCGCGGAGGTCAAGAACCCAGGGCC	426
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QY	427	TCAATCAAAAGTGCCTTAAGAGTACGGGCTATTTTCTTAATTAATGATTAAG	486
Db	841	TCAATGAAGATGTCTGCAAGGCTCTCGGTACACTTTCACAGCTACTGGATGACATGG	900
QY	487	GTGCGTAAAGCCCCCGGCGAGGCTGGAATGGATGGATCTTAACGGGCTCTGT	546
Db	901	ATATAACAGAGGCTGTGACAGGGTCTGGAGTSGATTTGTGCTATTTGATCTCGAAATAGT	960
QY	547	AGCACCGAATATACCGAAATTTTAAAGACCGTGTACTATGACGGGTGACACTTCGACT	606
Db	961	GATACATATTACAACCGGCAATTCAAACACAAAGCCAAACTGACGTGACATCTCCACC	1020
QY	607	AGTACGATATACATGAGCTCTCCAGCTTGCCATCGGAGAGACAGGGCCTCTATTTATTC	666
Db	1021	AGCACTCCCTACATGAGCACTCAACAGCTGACAAATAGAGACTCTGGGCTATTACTGT	1080
QY	667	GGCGCTATTTTT 679	
Db	1081	ACCCCTCTTATTT 1093	

RESULT 14
US-08-230-843-3
; Sequence 3, Application US/08230843
; Patent No. 5582826
; GENERAL INFORMATION:

1 APPLICANT: SHIMAMURA, TOSHIRO
2 APPLICANT: HAMURO, JUNJI
3 APPLICANT: NAKAZAWA, HARUMI
4 APPLICANT: KANAYAMA, YUKA
5 APPLICANT: SUGAMURA, KAZUO
6 APPLICANT: TAKESHITA, TOSHIKAZU
7 TITLE OF INVENTION: IMMUNOSUPPRESSANT
8 NUMBER OF SEQUENCES: 12
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
11 ADDRESSEE: P.C.
12 STREET: 1755 S. Jefferson Davis Highway, Suite 400

```

:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: Patent In Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/230,843
FILING DATE: 21-APR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 094491/199
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 036065/199
FILING DATE: 02-MAR-1994

1 FILING DATE: 07-MAR-1994
2
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Oblon, No. 5582826man F.
5 REGISTRATION NUMBER: 24,618
6 REFERENCE/DOCKET NUMBER: 0010-0674-0X
7
8 TELECOMMUNICATION INFORMATION:
9
10 TELEPHONE: (703) 413-3000
11
12 TELEFAX: (703) 413-2220
13
14 TELEEX: 248855 OPAT UR

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? INFORMATION FOR SEQ ID NO: 3:
?
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 729 base pairs
?     TYPE: nucleic acid
?     STRANDEDNESS: double
?     TOPOLOGY: linear
?
? MOLECULE TYPE: Other nucleic acid
?
? FEATURE:
?     NAME/KEY: CDS

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LOCATION: 1..725
; TS-08-230-843-3

Query Match	33.5%	Score 250;	DB 1;	Length 725;
Best Local Similarity	60.9%	Pred. No. 2.5e-70;		
Matches 447: Conservative	0:	Mismatches 275:	Indels 12:	Gaps 2

Qy	67	ATCACCTCGGGCGCCAGCGGAAAACATCTATGCGCGCTGAACTGGTATCAACGTAAACCT	127
Db	64	ATCACATCTCGACGACAGTGGGAATTTTTCACATTTATTTAGCATGGTATACGACGAAACAG	122
Qy	127	GGGAAAGCTCGGAAGCTTCTGATTATACGGTGGCGAGCACTGGCGAGATGGAGATCCCTTCT	184
Dy	124	GGAAATATCTCTACAGCTCTGGTCTATATATCGAAAAACCTTAGCGAGATGGTGCATCA	181
Qy	184	GGGAAAGCTCGGAAGCTTCTGATTATACGGTGGCGAGCACTGGCGAGATGGAGATCCCTTCT	241
Dy	181	GGAAATATCTCTACAGCTCTGGTCTATATATCGAAAAACCTTAGCGAGATGGTGCATCA	238

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 20:36:42 ; Search time 1890.83 Seconds

(without alignments)
707.902 Million cell updates/sec

Title: US-08-487-283a-12

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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82: gb_v12:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	478.2	63.8	1599	9 HUMICHEPAH	M87789 Human (hybr
2	476	63.5	9209	5 AR000007	AR000007 Sequence
3	476	63.5	9209	5 AR015961	AR015961 Sequence
4	476	63.5	9209	5 AR060920	AR060920 Sequence
5	476	63.5	18986	5 AR051652	AR051652 Sequence
6	467.4	62.3	3282	5 AR038306	AR038306 Sequence
7	467.4	62.3	3282	5 AR038320	AR038320 Sequence
8	467.4	62.3	3282	5 I58595	I58595 Sequence 15
9	467.4	62.3	3282	5 I58609	I58609 Sequence 16
10	467.4	62.3	13254	5 AR038307	AR038307 Sequence
11	467.4	62.3	13254	5 AR038321	AR038321 Sequence
12	467.4	62.3	13254	5 I58596	I58596 Sequence 15
13	467.4	62.3	13254	5 I58610	I58610 Sequence 17
14	459.6	61.3	762	5 I59485	I59485 Sequence 57
15	459.6	61.3	762	5 I73104	I73104 Sequence 57
16	459.6	61.3	762	5 I79289	I79289 Sequence 57
17	459.6	61.3	762	5 I87063	I87063 Sequence 57
18	453.8	60.5	2178	5 AR048108	AR048108 Sequence
19	453.8	60.5	2178	5 AR054190	AR054190 Sequence
20	447.2	59.6	671	39 AF051100	AF051100 Homo sapi
21	443.2	59.1	687	5 I65402	I65402 Sequence 1
22	442.2	59.0	6557	5 I26929	I26929 Sequence 3
23	435.4	58.1	666	9 AB022655	AB022655 Homo sapi
24	432.8	57.7	756	5 I69461	I69461 Sequence 29

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25 432.8 57.7 756 5 I73080 Sequence 29
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27 432.8 57.7 756 5 I87039 Sequence 29
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29 431.6 57.5 1404 5 A99058
30 431.6 57.5 2133 5 A99081
31 427 56.9 675 9 HUMIGGVHX
32 425.4 56.7 803 9 HUMGIIIA
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ALIGNMENTS

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RESULT 1
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DEFINITION Human (hybridoma H210) anti-hepatitis A IgG variable region,
constant region, complementarity-determining regions mRNA, complete
cds:
ORIGIN
M87789
M87789.1 GI:185361
complementarity-determining region; constant region; immunoglobulin
gamma-chain; immunoglobulin heavy chain; variable region.
Homo sapiens cDNA to mRNA.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1599)
Lewis,A.P., Lemon,S.M., Barber,K.A., Murphy,P., Parry,N.R.,
Peakman,T.C., Sims,M.J., Worden,J. and Crowe,J.S.
Rescue, expression, and analysis of a neutralizing human
anti-hepatitis A virus monoclonal antibody
J. Immunol. 151 (5), 2829-2838 (1993)
93367243
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Best Local Similarity 78.0%; Pred. No. 7.6e-103;
Matches 595; Conservative 0; Mismatches 153; Indels 15; Gaps 1;
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Db 155 TGAAGCATCTGGAGGCGCTTTCAGCACTATGCTATCAGCTGGTGGCAGAGGCCCT 214
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QY 466 TCCAAGAGCACCTCTGGGGCACAGCGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 525
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QY 526 GAACCGGTGACGCTGTCTGGAACCTCAGGCGCGCTGACACAGCGCGCTGACACCTTCCCG 585
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QY 586 GCTGTCTCAGTCTCAGGACTCTACTCTCCTCAGCAGCGTGGTGGTGGTGGTGGTGGTGGT 645
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RESULT 2
LOCUS AR000007 9209 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 3 from patent US 5736137.
ACCESSION AR000007
VERSION AR000007.1 GI:3962538
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9209)
AUTHORS Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Refl,M.E. and Rastetter,W.H.
TITLE Therapeutic application of chimeric and radiolabeled antibodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma
JOURNAL Patent: US 5736137-A 3 07-APR-1998;
FEATURES Location/Qualifiers
source 1..9209
BASE COUNT 2239 a 2397 c 2390 g 2183 t
ORIGIN

Query Match 63.5%; Score 476; DB 5; Length 9209;
Best Local Similarity 78.2%; Pred. No. 2.5e-102;
Matches 385; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 ATGAAGTGAAGCTGGGTATCTCTCTCTGTCAGTACAGCGGCGCTCCACCA 60
DB 2401 ATGGGTGAGACCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
QY 61 GTCCACTGTGCAATCCGGCGGAGGTCAAGAACGAGGCGCTCAGTCAAGTGTCC 120
DB 2461 GTACAACTGACAGACCTGGGCGTGAAGCTGGAGCGCTCAGTGAAGATGTCC 2520
QY 121 TGTAAAGTGAAGCTGGGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 2521 TGTAAAGTGAAGCTGGGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2580
QY 181 GGGCAGGCGCTGGAATGATGGGTGAGATCTTACCGGCTCGGTGAGACCGAATATACC 240
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QY 481 GGGGCGACAGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
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DB 2998 TCAGAGCTTACTCCCTCAGCAGCGGTGTGACCGGTGCTCCAGCAGCTTGGGACACCG 3057
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DB 3058 ACTCATCTGCAAGCTGATCAAGACCCAGCAACCAAGGTGAGCAAGAAAGTGTAG 3117
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LOCUS AR015961 9209 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5776456.
ACCESSION AR015961
VERSION AR015961.1 GI:3972238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9209)
AUTHORS Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Refl,M.E. and Rastetter,W.H.
TITLE Therapeutic application of chimeric and radiolabeled antibodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma
JOURNAL Patent: US 5776456-A 2 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..9209
BASE COUNT 2238 a 2395 c 2394 g 2182 t
ORIGIN

Query Match 63.5%; Score 476; DB 5; Length 9209;
Best Local Similarity 78.2%; Pred. No. 2.5e-102;
Matches 385; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 ATGAAGTGAAGCTGGGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
DB 2401 ATGGGTGAGACCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
QY 61 GTCCACTGTGCAATCCGGCGGAGGTCAAGAACGAGGCGCTCAGTCAAGTGTCC 120
DB 2461 GTACAACTGACAGACCTGGGCGTGAAGCTGGAGCGCTCAGTGAAGATGTCC 2520
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DB 2521 TGTAAAGTGAAGCTGGGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2580
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	Best Local Similarity	78.7%;	Pred. No. 2.7e-100;	
	Matches 577;	Conservative	0; Mismatches 141;	Indels 15; Gaps
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Db	3268	ATGGATATGGAGGTGGGTCTTTCTCTCTCTCCTGCTAGTACTACAGTGATCCACTCCAG	3209	
OY	61	GTCCAACTGGTGCCAATCCGGCCCCGAGGTCAAGAAGCACGGGGCCTCACTCAAAGTGCC	120	
Db	3208	GTTTCAGCTGGTTTCAGTCCCGGGCTGAGGTGAAGAAGCCCTGGGGCCTCATGTGAAGTTTCT	3149	
OY	121	TGTAAGCTAGAGGGGATATTTTTTCTATTATTATTTGATTCAATGGGTGGTCCAGCCCC	180	
Db	3148	TGTCAGGCTCTGTGATACGATTCAGTAACTTTGTTATTTCATTTGGGTGGCGCAGGCCCCC	3089	
OY	181	GGGCAGAGGCTCGAATGATGAGGTGGTGAATCTTACC GGCGCTGTGTAGCACCAATAATACC	240	
Db	3088	GGACAGAGGTTTGAGTGAATGGGATNGATNCATCTCTTACAAGGAAACAAAGAAATTTTCA	3029	
OY	241	GAAAAATTTTAAAGCCGTGTACTATGACCGGTGACACTTTCAGTACTAGTATATACATG	300	
Db	3028	GCGAAGTTCACAGACAGATCTACCTTTACCGGGGACACATCCGCAACACAGCTATACATG	2969	
OY	301	GAGCTCTCCAGCTCGATCCGAGGAGACACGGCGCTATATTGGCG-----	348	
Db	2968	GAGTTGAGAGGCTCAGGCTCTGACGACAGCGGTATTATTATGTGCGAGACTGGGCCCA	2909	
OY	349	--CGTATATTTTGGTGTCTAGCCCGAATGTGATTTTGGATGTTGGGGTCAAGGAACC	405	
Db	2908	TATPATTTGGGATGATTTCTCCCAAGACAAATTATATATGAGACTCTGGGGCAAAGAAC	2849	
OY	406	CTGTGCTACTGTCTCGAGCGCTTCACCAAGGGGCCCATCGCTTCCCGCTGGCGCCTCC	465	
Db	2848	ACGGTCATCTGTAGCTACACTTCCACCAAGGGGCCCATCGTCTTCCCGCTGGCACCCCTCC	2789	
OY	466	TCCAGAGAGACTCTTGGGGGGCACAGCGCCCTGGGCTGCTGTGTCAAGACTACTTCCCG	525	
Db	2788	TCCAAGAGAGACTCTGGGGGGCACAGCGGCCCTGGGCTGCTGTCAAGAGACTACTTCCCG	2729	
OY	526	GAACCGGTACCGGTGTCGTGGAACACTCAGGCGGCCCTGACAGCGGGCGTGACACTTCCCG	585	
Db	2728	GAACCGGTACCGGTGTCTGTGGAACACTCAGGCGGCCCTGACAGCGGGCGTGACACTTCCCG	2669	
OY	586	GCTGTCTCACTAGTCTCTCAGAGACTTACTCTCCCTCAGCAGAGCGTGTGACCGTGCCTCCAC	645	
Db	2668	GCTGTCTCTCACTAGTCTCTCAGAGACTTACTCTCCCTCAGAGAGGTGTGACCGTGCCTCCAC	2609	
OY	646	AGCTTGGGCAACCAAGACTTACATCTGTGCAACGTGAATCACAAAGCCAGCAACCAAGGTG	705	
Db	2608	AGCTTGGGCAACCAAGACTTACATCTGTGCAACGTGAATCACAAAGCCAGCAACCAAGGTG	2549	
OY	706	GACAGAAAGTTG 718		*
Db	2548	GACAGAAAGTTG 2536		
	RESULT 10			
	AR038307			
LOCUS	AR038307	13254 bp	DNA	PAT 29-SEP-1999
DEFINITION	Sequence 156 from patent US 5804440.			
ACCESSION	AR038307			
VERSION	AR038307.1	GI:5957024		
KEYWORDS	.	Unknown.		
SOURCE	Unknown.	Unknown.		
ORGANISM	Unclassified.			

REFERENCE	(bases 1 to 13254)
AUTHORS	Burton,D.R., Barbas,C.F. and Lerner,R.A.
TITLE	Human neutralizing monoclonal antibodies to human immunodeficiency virus
JOURNAL	Patent: US 5804440-A 156 08-SEP-1998;
FEATURES	Location/Qualifiers
SOURCE	1..13254 /organism="unknown"
BASE COUNT	3206 a 3559 c 3251 g 3238 t
ORIGIN	
Query Match	62.3%; Score 467.4; DB 5; Length 13254;
Best Local Similarity	78.7%; Pred.No.2.7e-100;
Matches 577; Conservative	0; Mismatches 141; Indels 15; Gaps 1.
1	ATGAAGTGAAGTGGAGTTAATCTCTCCCTCCGTGCTAGTACAGCGCGGCTCCACATCCCAA 60
Db	2450 ATGGAATGAGAGCTGGGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 2509
QY	61 GTCCAATGCTGTCATTCGCGCGCCGAGGTCAAGAAACCGAGGCGCTCACTCAAAAGTCCG 120
Db	2510 GTTCAGCTGTTACAGCCGGCGGTGAGTGAAGAAAGCCTGGGGCCTCACTGAAGGTTCT 2569
QY	121 TGTAAAGCTACGCGCTATATTTTCTTAATTATGATTCATAGGTGCTCAGGCCCCC 180
Db	2570 TGTACGGCTCTCGGATACAGATTCACTTGTATTATTCATTGGGTGGCGCGGCCCCC 2629
QY	181 GGGCAGGCGCTGGAATGATGGGTGAGATCTTACCGGGCTGTGTGACACCGAATATACC 240
Db	2630 GCACAGAGTTGATGTGATGGATGGATGATCAATCCTTACACAGGAACAAAGATTTTCA 2689
QY	241 GAAAAATTTTAAAGCCGTGTTACTATGACGCGTGACCTTGCAGTACTAGTATACATG 300
Db	2690 GCGAAGTTCAGAGACAGAGATCACTTACCGGGAGACATCCGGGCAACAGCTACATG 2749
QY	301 GAGCTCTCCAGCCTCGCATCGAGACACGCGCTATATTTATTTGCGCG----- 348
Db	2750 GAGTTGAGAGGCTCAGGTCTGCAGACACGCGCTTATTTATTTGTCGAGAGTGGGCCA 2809
QY	349 ---CGTATTTTGGTGTCTAGCCCGAATGATTTGATGTTGGGGTCAAGGAACC 405
Db	2810 TATAGTGGATGATTTCTCCCAAGCAATTTATATGAGCTGTGGGGCAAAAGGAACC 2869
QY	406 CTGTCTACTGTCTCGAGCCCTTCACAAAGGGCCCATCGTCTTCCCGCTGGGCGCTCC 465
Db	2870 AAGGTCATGTAGCTCAGCTTCAACAAAGGGCCCATCGTCTTCCCGCTGGGCGCTCC 2929
QY	466 TCCAAAGACACTCTGGGGGGCACAGCGGCGCTGGGCTGCTGTCAGGACTACTTCCCC 525
Db	2930 TCCAAAGACACTCTGGGGGGCACAGCGGCGCTGGGCTGCTGTCAGGACTACTTCCCC 2989
QY	526 GAACGGGTGACGCTGTCGGAATCAGGCGGCTGACAGGGGCTGACACACTTCCCG 585
Db	2990 GAACGGGTGACGCTGTCGGAATCAGGCGGCTGACAGGGGCTGACACACTTCCCG 3049
QY	586 GGTGTCTCTACACTCTCAGAGACTACTCTCCCTCAGAGCGGTGGTGAACCTGACCTCCAC 645
Db	3050 GGTGTCTCTACACTCTCAGAGACTACTCTCCCTCAGAGCGGTGGTGAACCTGACCTCCAC 3109
QY	646 AGCTTGGGACCCAGACCTACTCTGCAACGTGAATCACAAGCCCAACCAAGAGGTG 705
Db	3110 AGCTTGGGACCCAGACCTACTCTGCAACGTGAATCACAAGCCCAACCAAGAGGTG 3169
QY	706 GACAAAGAAAGTTG 718
Db	3170 GACAAAGAAAGTTG 3182


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Db 3110 AGCTGGGACCCACAGCTACATCTGCAACGTGAATCACAAGCCCAAGCAACAGAGTG 3169
Qy 706 GACAAGAAAGTTG 718
Db 3170 GACAAGAAAGTTG 3182

RESULT 13
LOCUS 158610 13254 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 170 from patent US 5652138.
ACCESSION 158610
VERSION 158610.1 GI:2477848
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13254)
AUTHORS Burton,D.R., Barbash,C.F. and Lerner,R.A.
TITLE Human neutralizing monoclonal antibodies to human immunodeficiency
virus
JOURNAL Patent: US 5652138-A 170 29-JUL-1997;
FEATURES
SOURCE Location/Qualifiers
BASE COUNT 3238 a 3251 c 3559 g 3206 t
ORIGIN

Query Match 62.3%; Score 467.4; DB 5; Length 13254;
Best Local Similarity 78.7%; Pred. No. 2.7e-100;
Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps 1;

Qy 1 ATGAAGTGGAGCTGGGTTATCTCTCTCTCTGTCAGTACTGCCGGCTGCACCTCCAA 60
Db 10805 ATGGAATGAGCTGGGCTTCTCTCTCTCTCTGTCAGTACTGCCGGCTGCACCTCCAA 10746
Qy 61 GTCCAACTGCTGCAATCCGGGCCAGAGTCAGAAAGCCAGGGGCTCATCAAGTGTCC 120
Db 10745 GTTACGCTGCTGCAATCCGGGCCAGAGTCAGAAAGCCAGGGGCTCATCAAGTGTCT 10686
Qy 121 TGTAAAGCTACGCTATATTTTCTATATATGATCAATGGGCTGCTGAGGCCCC 180
Db 10685 TGTCAAGCTTCTGATACAGATTCAGTACTTGTATTATTCATGGGCTGCTGAGGCCCC 10626
Qy 181 GGGCAGGGCTGGAATGGATGGGTAGATCTTACCGGGCTCTGTAGACCAACCAATATAC 240
Db 10625 GGACAGAGTTGATGATGGATGGATGATCAATCTTACCAAGCAACCAAGATTTTCA 10566
Qy 241 GAAATTTTAAAGACCGTGTACTATGACGCTGACACTTGCATAGTACAGTATCATG 300
Db 10565 GCGAAGTCCAGGACAGAGTACCTTACCGGACACATCCGCAACACAGCTACATG 10506
Qy 301 GAGCTCTCAGCTGCGATCGGAGGACAGCGGCTCTATTTATTTGGCG----- 348
Db 10505 GAGTGTAGAGACCTCAGCTCTGACAGACAGGCTGTTTATTATTTGTCGAGATGGGCCA 10446
Qy 349 ---CGTATTTTGTGTTCTAGCCGGAATTTGATTTTGTGTTGGGTCAGAGAAC 405
Db 10445 TATAGTTGGATGATTTCTCCAGAGCAATATTTATGAGAGCTGTGGGGCAAGGAAC 10386
Qy 406 CTGTGCTACTGCTGACGCGCTCCACCAAGGCCCAATGGGTCTTCCCTGGCGCCCTCC 465
Db 10385 ACGGTCACTGCTGAGCTGCTCCACCAAGGCCCAATGGGTCTTCCCTGGCGCCCTCC 10326
Qy 466 TCCAAGACACACTCTGGGGGACACAGGGCCCTGGGGCTGCTGCTGAAGACTACTGCCCC 525
Db 10325 TCCAAGACACACTCTGGGGGACACAGGGCCCTGGGGCTGCTGCTGAAGACTACTGCCCC 10266
Qy 526 GAACCGGTGACGCTGCTGGAATCAGAGCCCTGACAGGCGGTGACACACTTCCCG 585
Db 10265 GAACCGGTGACGCTGCTGGAATCAGAGCCCTGACAGGCGGTGACACACTTCCCG 10206

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Qy 586 GCTGTCTTACAGTCTCTCAGAGCTCTACTCCCTCAGACAGCGTGGTGAACCTGCCACAGC 645
Db 10205 GCTGTCTTACAGTCTCTCAGAGCTCTACTCCCTCAGACAGCGTGGTGAACCTGCCACAGC 10146
Qy 646 AGCTTGGCACCACCAAGCTTACATCTGCAACGTGAATTCACAGCCCAACCAAGGTG 705
Db 10145 AGCTTGGCACCACCAAGCTTACATCTGCAACGTGAATTCACAGCCCAACCAAGGTG 10086
Qy 706 GACAAGAAAGTTG 718
Db 10085 GACAAGAAAGTTG 10073

RESULT 14
LOCUS 169485 762 bp DNA PAT 04-FEB-1998
DEFINITION Sequence 57 from patent US 5677426.
ACCESSION 169485
VERSION 169485.1 GI:2831607
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 762)
AUTHORS Fong,S., Hebert,C.Alice, Kim,K.Jin and Leong,S.R.
TITLE Anti-IL-8 antibody fragments
JOURNAL Patent: US 5677426-A 57 14-OCT-1997;
FEATURES
SOURCE Location/Qualifiers
BASE COUNT 183 a 224 c 186 g 169 t
ORIGIN

Query Match 61.3%; Score 459.6; DB 5; Length 762;
Best Local Similarity 76.8%; Pred. No. 1.9e-98;
Matches 561; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

Qy 21 TCTCTTCTCTCTGTCAGTAACTCCCGGCTGCACCTCCCAAGTCCAACTGTCGAATCCG 80
Db 33 TATGTTCTTTTCTTATTTCTACAAACGCGTACGCTGATTCAGCTGCAGCAGTCTGG 92
Qy 81 CCGCGAGTCAAGAAACCAAGGGGCTCTACATCAAGTGTCTGTAACTGACCGCTATAT 140
Db 93 ACCTGAGCTGATGAACCTGGGGCTTCAAGTGAATATCTGGAAGGCTTCTGTATATTC 152
Qy 141 TTTTCTAATTTATGATTCATGAGGTGCTGACAGCCCGGCGAGGAGCTGGATATGAT 200
Db 153 ATTCAGTACGCACTACATGACACTGGGTGAAGCAGAGCCATGAAAGACCTTGATGATG 212
Qy 201 GGGTGAATCTTACCGGGCTCTGTAGACCAAGATATACGAAATTTTAAAGACCGTGT 260
Db 213 TGGCTCATGATGATCTTCCAAATGTTGAATGATCTTACCAAGAAATTTCAAGGGCAAGG 272
Qy 261 TACTATAGACCGTGAACACTTCACTAGTACATGATACATGAGACTCTCAGCCTGAGAT 320
Db 273 CACATTGACGTGATGACACATCTTCCAGACAGCAACGTCATCTCAGCAGCTGACATC 332
Qy 321 GGAGACAGCGCGCTCTATATGATGCGGCTTATTTTGTGTTCTGAGCCGAATGGTA 380
Db 333 TGATGACTCTGCACTATTTCTGTGCAAGAGGGGACTATAGATACAAAGCCGCACTGTT 392
Qy 381 TTTTGAATTTGGGGTCAAGGAACCTGTGCTACATGCTCAGAGCCCTCCACCAAGGCC 440
Db 393 TTTGATGCTGTGGGGGACAGAGGACACAGGTCACAGCTCTCCGCGCTCCACCAAGGGCC 452
Qy 441 ATGGTCTTCCCTGCGGCTCTCTCACAAGACACTCTGGGGGACACAGGCGCTTGG 500
Db 453 ATGGTCTTCCCTGCGGCTCTCTCACAAGACACTCTGGGGGACACAGGCGCTTGG 512
Qy 501 CTGCTGCTCAAGACTACTTCCCGGAACCGGTGAGGCTGCTGGAATCTCAGGCGCT 560

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Db 513 CTGCTGTCTAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCT 572
QY 561 GACCAGCGGCTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAG 620
Db 573 GACCAGCGGCTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAG 632
QY 621 CAGCGTGTGACCGTGTCCCTCAGCAGCTTGGGCAACCCAGACCTACATCTGCAAGGTGAA 680
Db 633 CAGCGTGTGACCGTGTCCCTCAGCAGCTTGGGCAACCCAGACCTACATCTGCAAGGTGAA 692
QY 681 TCACAAGCCCGAGCAACACAGGTGGCAAGAAAGTTGAGCCCAATCTTGTGACAAAAC 740
Db 693 TCACAAGCCCGAGCAACACAGGTGGCAAGAAAGTTGAGCCCAATCTTGTGACAAAAC 752
QY 741 TCACACATAA 750
Db 753 TCACACATGA 762

RESULT 15
I73104
LOCUS I73104 762 bp DNA PAT 03-APR-1998
DEFINITION Sequence 57 from patent US 5686070.
ACCESSION I73104
VERSION I73104.1 GI:3009243
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 762)
Doerschuk,C.M., Fong,S., Hebert,C.Alice, Kim,K.Jin and Leong,S.R.
TITLE Methods for treating bacterial pneumonia
JOURNAL Patent: US 5686070-A 57 11-NOV-1997;
FEATURES
source
1..762
BASE COUNT 183 a 224 c 186 g 169 t
ORIGIN
/organism="unknown"

Query Match 61.3%; Score 459.6; DB 5; Length 762;
Best Local Similarity 76.8%; Pred. No. 1.9e-98;
Matches 561; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 21 TCTTCTCTCTGTCAGTAACCTGCGGGGTCCACCTCCCAAGTCCAACTGGTGCATCCGG 80
Db 33 TATGTTCTGTTTTTCTATTGTACAAACGCGTACGCTGAGATTTCAGCTGCAGCAGTGG 92
QY 81 CGCGAGGTCAAGAAGCCAGGCGCTCAGTCAAAGTGTCTCTAAAGCTAGCGGCTATAT 140
Db 93 ACCTGAGCTGATGAAGCTTGGGGCTTCAGTGAAGATATCTCGAAGGCTTCTGGTTATTTC 152
QY 141 TTTTCTTAATTATTGGATTCAATGGTGGCTCAGGCGCCCGGCGAGGCGCTGGAATGGAT 200
Db 153 ATTCAAGTACCACTACATGCACTGGTGAAGCAGAGCCATGGAAAGAGCCTTGAAGTGGAT 212
QY 201 GGGTGAGATCTTACCGGGCTCTGGTAGCAGCCGAATATACCGAAATTTAAAGACCGTGT 260
Db 213 TGGCTACATTGATCTTCCAATGGTGAAGTACTTACACACCAAGAAATTCAGGGGCAAGGC 272
QY 261 TACTATGACGGGTGACACTTCGACTAGTACAGTATATACATGAGAGCTCTCCAGGCTCGGATC 320
Db 273 CACATTGACTGAGACATCTTCAGCAGACCCAGCTGCATCTCAGCAGGCTGACATC 332
QY 321 GGAGSACACGGCGCTATTATTATGGCGCGTTATTTTTTGGTTCTTAGCCCGAATTTGTA 380
Db 333 TGATGACTCTGCACTTATTTCTGTGCAAGAGGGGACTATAGATACACAGCGGACTGGTT 392
QY 381 TTTTGAATTTGGGGTCAAGAACCGCTGGTCACTGTCTCGAGGCGCTCCACCAAGGGCCC 440
Db 393 TTTTCGATGTCTGGGGCGCAGGACACCGGTCTCCCGGCTCTCCCGGCTCCACCAAGGGCCC 452
QY 441 ATCGGTCTTCCCGCTGGGCGCCCTCTCCAAAGAGCACCTCTGGGGGCGACAGCGGCCCTGGG 500

Db 453 ATCGGTCTTCCCGCTGGCACCCCTCTCCCAAGACACCTCTGGGGGCACAGCGCCCTGGG 512
QY 501 CTGCGCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCT 560
Db 513 CTGCGCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCT 572
QY 561 GACCAGCGGCTGCACACCTTCCCGGCTGTCTCTACAGTCTCAGGACTCTACTCCCTCAG 620
Db 573 GACCAGCGGCTGCACACCTTCCCGGCTGTCTCTACAGTCTCAGGACTCTACTCCCTCAG 632
QY 621 CAGCGTGTGACCGTGTCCCTCAGCAGCTTGGGCAACCCAGACCTACATCTGCAAGGTGAA 680
Db 633 CAGCGTGTGACCGTGTCCCTCAGCAGCTTGGGCAACCCAGACCTACATCTGCAAGGTGAA 692
QY 681 TCACAAGCCCGAGCAACACAGGTGGCAAGAAAGTTGAGCCCAATCTTGTGACAAAAC 740
Db 693 TCACAAGCCCGAGCAACACAGGTGGCAAGAAAGTTGAGCCCAATCTTGTGACAAAAC 752
QY 741 TCACACATAA 750
Db 753 TCACACATGA 762

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 20:04:48 ; Search time 930.19 Seconds
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3555.587 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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3	355	47.3	564	72	AW404758	UI-HF-BL0
4	352.8	47.0	581	71	AW378707	PM2-HT022
5	352.2	47.0	683	71	AW381291	RC0-HT029
6	346.4	46.2	475	72	AW403588	UI-HF-BK0
7	343.8	45.8	566	74	AW606291	QV0-HT036
8	341.2	45.5	527	72	AW402051	UI-HF-BK0
9	335.6	44.7	442	69	AW177689	RC1-CT019
10	333.6	44.5	634	74	AW606367	QV0-HT036
11	329.4	43.9	455	74	AW606325	QV0-HT036
12	322	42.9	579	72	AW403670	UI-HF-BK0
13	320.8	42.8	442	71	AW375944	RC0-CT020
14	318.8	42.5	504	72	AW403803	UI-HF-BK0
15	318.6	42.5	446	72	AW408074	UI-HF-BM0
16	318.6	42.5	518	72	AW402666	UI-HF-BK0
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19	316	42.1	522	46	AW1906070	RC-BT105-
20	314.4	41.9	602	71	AW383595	PM0-HT034
21	313.8	41.8	447	72	AW404044	UI-HF-BL0
22	309.6	41.3	350	71	AW378814	PM0-HT022
23	308.8	41.2	423	69	AW177695	RC1-CT019
24	308.2	41.1	414	74	AW606364	QV0-HT036
25	306	40.8	409	71	AW376081	RC2-CT020
26	304.6	40.6	409	72	AW406111	UI-HF-BL0
27	303.6	40.5	461	72	AW406952	UI-HF-BL0
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29	296.4	39.5	440	72	AW404734	UI-HF-BL0
30	295.4	39.4	463	72	AW406702	UI-HF-BL0
31	293.6	39.1	443	71	AW351514	IL2-CT003
32	293.2	39.1	432	46	AW1906265	AI906265
33	291.8	38.9	336	74	AW606317	QV0-HT036
34	287.4	38.3	620	71	AW379997	RC0-HT025
35	286.6	38.2	370	72	AW406413	UI-HF-BL0
36	284.8	38.0	513	71	AW380053	QV3-HT026
37	284.2	37.9	397	74	AW606343	QV0-HT036
38	280.4	37.4	513	72	AW402081	UI-HF-BK0
39	278.4	37.1	342	74	AW580270	IL2-HT043
40	278	37.1	361	74	AW609631	QV0-ST021
41	277.8	37.0	297	72	AW406093	UI-HF-BL0
42	277.6	37.0	358	72	AW405129	UI-HF-BL0
43	275.8	36.8	396	72	AW404187	UI-HF-BL0
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ALIGNMENTS

RESULT 1
LOCUS AW403676
DEFINITION UI-HF-BK0-abh-c-03-0-UI.r1 NIH_MGC_36 Homo sapiens CDNA clone
IMAGE:3056237 5', mRNA sequence.

AW403676
VERSION AW403676.1 GI:6922685
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 489)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL On Jun 15, 1998 this sequence version replaced gi:3224692.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES
Location/Qualifiers
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/clone="IMAGE:3056237"
/clone_lib="NIH_MGC_36"
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/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/notes="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 116 a 159 c 126 g 88 t
ORIGIN
Query Match 48.3%; Score 362; DB 72; Length 489;
Best Local Similarity 85.0%; Pred. No. 3.3e-92;
Matches 420; Conservative 0; Mismatches 65; Indels 9; Gaps 1;
QY 252 AGACCGTGTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGAGCTCTCCAG 311
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Db 5' AGCCGATTCACCAATCTCCAGAGACAATACAGAACACGCTGTATCTTCAATGAACAG 64
QY 312 CCTCGATCGGAGGACAGCGCGTCTAFTATTGGCGCGGTATTTTGGTTCCTAGGCC 371
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Db 65 CCTGAGACCGGAGGACAGCGCGTGTATTAATCTGCGAGAGAGGAGCGGAGTCCGATGC 124
QY 372 GAATGGTATTTGATGTTTGGGTCAGAGAACCCCTGTGCTACTGTCTGAGCGCCCTCCAC 431
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Db 125 -----TTTGTATATCTGGGCCCAAGGACAATGTCACCGTCTCTTCAGCCTCCAC 175
QY 432 CAAGGGCCCATCGGCTTCCTCCCTGGCGCCCTCCTCCAGAGACCTCTGGGGGACAGC 491
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Db 176 CAAGGGCCCATCGGCTTCCTCCCTGGCGCCCTCCTCCAGAGACCTCTGGGGGACAGC 235
QY 492 GGCCCTGGGCTGCCTTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAATC 551
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Db 236 AGCCCTGGGCTGCCTTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAATC 295
QY 552 AGGCGCCCTGACAGCGCGGTGCACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTA 611
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Db 296 AGGCGCCCTGACAGCGCGGTGCACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTA 355
QY 612 CTCCCTGACAGCGGTGGTGACCGTGCCTCCAGAGCTTGGGACCCAGACCTATATCTG 671
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Db 356 CTCCTCAGACAGCGTGTGACCTGCTCCCTCAGACAGCTTGGGACCCAGACCTACATCTG 415
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Qy 732 TGACAAACTCACA 745
Db 476 TGACAAACTCACA 489

RESULT 2
LOCUS AM606355 669 bp mRNA EST 23-MAR-2000
DEFINITION QV0-HTC366-280100-088-b12 HT0366 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM606355
VERSION AM606355.1 GI:7311096
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 669)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
On May 7, 1998 this sequence version replaced gi:3118821.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV06t2-QV0-HT0366-
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Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 661.
Location/Qualifiers
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/clone_lib="HT0366"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 160 a 191 c 185 g 133 t
ORIGIN
Query Match 47.8%; Score 358.4; DB 74; Length 669;
Best Local Similarity 73.8%; Pred. No. 3.7e-91;
Matches 493; Conservative 0; Mismatches 151; Indels 24; Gaps 2;
Qy 100 GGGGCGCTCAGTCAAGTGTCTCTGAAGCTAGCGGCTAATTTTCTAATTAATTGATT 159
Db 1 GGGGCGCTCCCGAGATCTCTGTGCACTCTGAGATTATTTTGTAGTAATACTAGAGAT 60
Qy 160 CATGGGTGCTCAGAGCCCGGCGAGGCGCTGGAATGATGGTGAATCTTACCGGGC 219
Db 61 GACCTGTGGTCCGAGGCTCCAGGAGGCGCTGAGAGGGGTGCGCAATATAGAGAGAT 120
Qy 220 TCTGTAGCAGCAGTAATACGAAATTTTAAGACCGGTGTACTATAGAGCGGTGACACT 279

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Db 121 GGAAGTGAACAACTATGTGGACTGTGTGAAGGGCCGATTCCACATCTCCAGGACAC 180
Qy 280 TCGAGTAGTACATATACATGAGCTCTCCAGCTGCGATGAGAGACGGCCGTAT 339
Db 181 GCCGAGAGTACTCTATCTGCAATATGACAGCCCTGAGAGGGGAGACAGCGCTGTATAT 240
Qy 340 TATTGCGCGC-----TTATTTTGTGTTCTAGCCGAAATG 377
Db 241 TACTGTGCGAGAGAAAAAAGGATGATAGCACTTTTGAATGGGTATCAAAACAAATGA 300
Qy 378 GTATTTGATGTTGGGTCAAGAACCTGTCTACTCTCTGAGCCCTCCACCAAGG 437
Db 301 TGTCTGATGTCGTGGGCGCAAGGACATGTGTCATCTCTTCCAGCTCCACCAAGG 360
Qy 438 CCCATGCTCTCCCGCTGGGCGCTCTCTCCAGAGACACTCTGGGGGACAGCGGCCCT 497
Db 361 CCCATGCTCTCCCGCTGGGCGCTCTCTCCAGAGACACTCTGGGGGACAGCGGCCCT 420
Qy 498 GGGCTGCTGTGCAAGACTCTCCCGAACCGGTGACGGTGTGGAATCAGGCGC 557
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Qy 558 CCTGACACGCGCGCTGCAACACTTCCGCGTGTCTCTACAGTCTCAGACTCTACTCCT 617
Db 481 CCTGACACGCGCGCTGCAACACTTCCGCGTGTCTCTACAGTCTCAGACTCTACTCCT 540
Qy 618 CAGAGCGTGTGACCGCTCCAGAGCTGTGGGACCCAGACTCTATCTGACACT 677
Db 541 CAGAGCGTGTGACCGCTCCAGAGCTGTGGGACCCAGACTCTATCTGACACT 600
Qy 678 GAATCACAAGCCCAAGCAACCAAGTGTGACAGAGATTGAGCCCAATCTTGTGACAA 737
Db 601 GAATCACAAGCCCAAGCAACCAAGTGTGACAGAGATTGAGCCCAATCTTGTGACAA 658
Qy 738 AACTCACA 745
Db 659 AATCACA 666

RESULT 3
LOCUS AM404758 564 bp mRNA EST 16-FEB-2000
DEFINITION UI-HF-BL0-acd-h-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058808 5', mRNA sequence.
ACCESSION AM404758
VERSION AM404758.1 GI:6923815
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 564)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNML at:
www-bio.lnl.gov/bhrp/image/image.html
Seq primer: M13 forward
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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FEATURES
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/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MG85"
/lab_host="DH10B (LTI)"

/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

119 a 210 c 138 g 97 t

BASE COUNT
ORIGIN

Query Match 47.3%; Score 355; DB 72; Length 564;

Best Local Similarity 84.8%; Pred. No. 3.3e-90;

Matches 413; Conservative 0; Mismatches 65; Indels 9; Gaps 1;

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Db 2 ACGAGGTACGGCCAGCAAGTCCATCAACACCGCTACCTGAGTGAGCAGCCTGAAGGCC 61

QY 322 GAGGACACGGCCTCTATTATTCGGCGCGTATTTTGGTCTTAGCCGAATTGGTAT 381

Db 62 TCGGACACGGCCATTATTACTGTGGAGACCCCT-----CAGCGGTGGCTGGGCC 112

QY 382 TTTGATGTTGGGTCAAGAACCTGGTCACTGCTCTGAGCGCTCCACCAAGGGCCCA 441

Db 113 CTGTGACTTGGGGCCAGGAACCTGGTCACTGCTCTGAGCGCTCCACCAAGGGCCCA 172

QY 442 TGGGTCTTCCCTCGCGCCCTCTCAAGAGCACCTCTGGGGCAGAGGGCCCTGGGC 501

Db 173 TCGGTCTTCCCTCGCGCCCTCTCAAGAGCACCTCTGGGGCAGAGGGCCCTGGGC 232

QY 502 TGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGCTGCTGGAAGTCAAGCGCCCTG 561

Db 233 TGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGCTGCTGGAAGTCAAGCGCCCTG 292

QY 562 ACCAGGGGGTGACACCTTCCCGGCTGCTCTACAGTCCCTCAGGACTCTACTCCCTCAGC 621

Db 293 ACCAGGGGGTGACACCTTCCCGGCTGCTCTACAGTCCCTCAGGACTCTACTCCCTCAGC 352

QY 622 AGCGTGGTACCGTGCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAAGTGAAT 681

Db 353 AGCGTGGTACCGTGCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAAGTGAAT 412

QY 682 CACAAGCCAGCAACCAAGGTGGACAAGAAAGTTGAGCCCAATCTTGACAAAACT 741

Db 413 CACAAGCCAGCAACCAAGGTGGACAAGAAAGTTGAGCCCAATCTTGACAAAACT 472

QY 742 CACACAT 748

Db 473 CACACAT 479

RESULT 4

AW378707 AW378707 581 bp mRNA EST 04-FEB-2000
LOCUS PM2-HT0225-031299-003-b01 HT0225 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION AW378707
VERSION AW378707.1 GI:6883366
KEYWORDS EST.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 581)

REFERENCE HCGP <http://www.ludwig.org.br/ORESTES>.

AUTHORS The FAPESP/LICR Human Cancer Genome Project

TITLE Unpublished (1999)

JOURNAL On Feb 10, 1999 this sequence version replaced gi:4061421.

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpon@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-HT0225-031299-003-b01&t3=1999-12-03&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 13

High quality sequence stop: 575.

Location/Qualifiers

FEATURES

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HT0225"

/dev_stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

113 a 189 c 160 g 119 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 427; Conservative

QY 163 TGGGTGCGTCAGGCCCCCGGCGAGGCTTGAATGGATGGGTGAGATCTTACCGGCTCT 222

Db 45 TGGGTGCGGACGCGCCCTGGACAAGGCTTGGTGGTGGGAAGATATTCCTTTGGCT 104

QY 223 GGTAGCACGATATACCGAAATTTTAAAGACCTGTACTATGACGGTGACACTTCG 282

Db 105 GGTATCGGATCTACGGTAAGAAATTCCTGGACAGAATCACAAATTACCGGACATGTCT 164

QY 283 ACTAGTACAGTATACATGGAGCTCTCCAGCTCGGAGGACGAGGCGGCTCTATTAT 342

Db 165 GCGCCACAGCCTCTTGGAGGTGACAACTCCGATCTGAGGACACGCGGCTCTACTAC 224

QY 343 TCGCGCGCTTATTTTGGTTCTAGCCCGAATTTGGTATTTTGTGTTGGGGTCAAGA 402

Db 225 TGTGTGCGCATAGAAGTGGTGACAATC---TTGCACCTTTTGTGTTGGGGCTCGGA 281

QY 403 ACCCTGGTCACTGCTCGAGGCGCTCCACCAAGGCGCCATCGGCTTCCCTCTGGGCGCC 462

Db 282 ACTTCCGTCACCGTCTCTGACGCTCCACCAAGGCGCCATCGGCTTCCCTCTGGCACC 341

QY 463 TCCTCCAAGAGCACCTCTGGGGGACAGCGGCTGGCTGCTGGTCAAGGACTACTTC 522

Db 342 TCCTCCAAGAGCACCTCTGGGGGACAGCGGCTGGCTGCTGGTCAAGGACTACTTC 401

QY 523 CCGGAACCGGTGACGGTGTGTTGGAACCTCAGCGGCGCTGACAGCGGCTGACACCTTC 582

Db 402 CCCGAACCTGGTGACGGTGTGTTGGAACCTCAGCGGCGCTGACAGCGGCTGACACCTTC 461

QY 583 CCGGTCTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGGCTGGTGCCTGCTCC 642

Db 462 CCGGTCTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGGCTGGTGCCTGCTCC 521

QY 643 AGCAGCTTGGGCGCCAGACCTTACATCTGCAACGTGAATCAACAAGCCAGCA 694

Db 522 AGCAGCTTGGGCGCCAGACCTTACATCTGCAACGTGAATCAACAAGCCAGCA 573

RESULT 5

AW381291

LOCUS

AW381291

683 bp mRNA EST

04-FEB-2000

DEFINITION	RCO-HT0298-2011199-011-f08 HT0298 Homo sapiens cDNA, mRNA sequence.
ACCESSION	AM81291
VERSION	AM81291.1 GI:6885950
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 683)
TITLE	HCFP http://www.ludwig.org.br/ORESTES .
JOURNAL	The FAPESP/LICR Human Cancer Genome Project
COMMENT	Unpublished (1999) On May 18, 1998 this sequence version replaced gi:3136800. Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC0&t2=RC0-HT0298-201199-011-f08&t3=1999-11-20&t4=1) Seq primer: puc 13 forward High quality sequence start: 15 High quality sequence stop: 657. Location/Qualifiers
FEATURES	1..683 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HT0298" /dex_stage="Adult" /note="Organ: head/neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT	146 a 224 c 181 g 132 t
ORIGIN	
Query Match	47.0%; Score 352.2; DB 71; Length 683;
Best local Similarity	86.6%; Pred. No.2.2e-89;
Matches 401; Conservative	0; Mismatches 58; Indels 4; Gaps 1;
OY	290 CAGTATACATGAGAGCTCCACACCTGCATCGAGAGACAGCGCCGCTATTATTA-r--TTGC 345
Db	6 CACGTATCTGCAATGAACACAGCTCGAAGAGCTGAGAGACACGGCTGTGATTACTTGTCGC 65
OY	346 GCGCGTATTTTTTTGGTTTAGCCCGAATGGTATTTGATGTTGGGGTCAAGAAAC 405
Db	66 CCACGCCCTTATGATAGTAGTGGTATTCTTACTACGTTTGACTAGTGGGCCAGGAAC 125
OY	406 CTGGCTACTGTCGAGGGCCACACCAAGAGGCCCATGGTCTTCCCGCCGCCCTCC 465
Db	126 CTGGTCACCGTCCCTCAGCTTCCACCAAGGGCCCATGGTCTTCCCGCCGCCCTGC 185
OY	466 TCACAAGACACCTCTGGGGGACACAGGCCCTGGGGCTGCTGTCACAAGACTATTC 525
Db	186 TCACAGACACTCTCTGGGGGACACAGGCCCTGGGGCTGCTGTCACAAGACTATTC 245
OY	526 GAACCGGTGACGGTCTGTGAACCTCAGGCGCCCTGACCAAGCGGCGTCCACACTTCCG 585
Db	246 GAACCGGTGACGGTCTGTGAACCTCAGGCGCCCTGACCAAGCGGCGTCCACACTTCCG 305
OY	586 GCTGTCACAGTCTCTCAGAGACTACATCCCTCAGACAGGTGATACCGTGCCTCCAGC 645
Db	306 GCTGTCACAGTCTCTCAGAGACTACATCCCTCAGACAGGTGATACCGTGCCTCCAGC 365

QY	646	ACCTGGGGACCCACACACCTACATCTCGCAACCGTGATCAACAAGCCACGACACCAAGGTG	705
DB	366	ACCTGGGGACCCACACACCTACATCTCGCAACCGTGATCAACAAGCCACGACACCAAGGTG	425
QY	706	GACAAAGAAAGTTGAGCCCAATCTTGTCGCAAAAGTCAACAT	748
DB	426	GACAAAGAGTTGAGCCCAATCTTGTCGCAAAAGTCAACAT	468
RESULT	6		
AM403588			
LOCUS			
DEFINITION	AM403588	475 bp	mRNA
ACCESSION	AM403588		EST
VERSION	AM403588.1		16-FEB-2000
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 475)		
JOURNAL	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	Eco RI site shown at the beginning of the sequence.		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
	cDNA Library Preparation: M.B. Soares Lab		
	cDNA Library Arrayed by: M.B. Soares Lab		
	DNA Sequencing by: M.B. Soares Lab		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/ILMN at:		
	www.bio.lnlnl.gov/bbrp/image/image.html		
	Seq primer: M13 Forward.		
FEATURES			
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	/cell_line="MGC85"		
	/lab_host="DH10B (lri)"		
	/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;		
	Constructed from size fractionated cytoplasmic mRNA		
	(0.5-1.5kb). Directionally cloned. Cells provided by Louis		
	M. Staudt, Ph.D. Library preparation by Maria de Fatima		
	Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
BASE COUNT	101 a	179 c	116 g
ORIGIN			79 t
Query Match	46.2%;	Score 346.4;	DB 72; Length 475;
Best Local Similarity	94.5%;	Pred. No. 8.7e-88;	
Matches 359;	Conservative	0;	Mismatches 21; Indels 0; Gaps 0;
QY	369	CCCGAATTGGTATTTTGTATGTTGGGGGTCAAGAAACCTGTCAGTCTCGAGCGCTC	428
DB	1	CACGAGGGGCTCAATGAGAGTCTGGGGGCAAAAGGACACAGGTCACCGTCTCTCAGCGCTC	60
QY	429	CACCAAGGGGCCATGGGTTCCCGCTGGCGGCTCTCCAGAGACACCTCTGGGGGAC	488
DB	61	CACCAAGGGGCCATGGGTTCCCGCTGGCGGCTCTCCAGAGACACCTCTGGGGGAC	120
QY	489	AGCGGCGCTGGGCTCTGTCGTAAGAGACTACTCCCGAAGCGGTGACGGTCTGTGGA	548
DB	121	AGCGGCGCTGGGCTCTGTCGTAAGAGACTACTCCCGAAGCGGTGACGGTCTGTGGA	180
QY	549	CTCAGGCGCCTGACCAAGCGGCTGACACCTTCCCGGCTGTCTACAGTCTCAGACT	608

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QY 609 CTACTCCCTCAGCAGCGTGGTACCGTCCCTCAGCAGCTTGGGACCCAGACCTACAT 668
Db 241 CTACTCCCTCAGCAGCGTGGTACCGTCCCTCAGCAGCTTGGGACCCAGACCTACAT 300
QY 669 CTGCAACGTGAATCAAGCCAGCAGCAACACCAAGGTGGACAAAGTTGAGCCCAATC 728
Db 301 CTGCAACGTGAATCAAGCCAGCAGCAACACCAAGGTGGACAAAGTTGAGCCCAATC 360
QY 729 TTGTGACAAAACCTCACACAT 748
Db 361 TTGTGACAAAACCTCACACAT 380

RESULT 7
LOCUS AW606291 566 bp mRNA EST 23-MAR-2000
DEFINITION QV0-HT0366-270100-087-a02 HT0366 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW606291
VERSION AW606291.1 GI:7311032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE HCGP http://www.ludwig.org.br/ORESTES.
JOURNAL The FAPESP/LICR Human Cancer Genome Project
COMMENT Unpublished (1999)
On Jun 15, 1998 this sequence version replaced gi:3224227.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-HT0366-
270100-087-a02&t3=2000-01-27&t4=1)
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High quality sequence start: 21
High quality sequence stop: 566.
Location/Qualifiers
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/clone_lib="HT0366"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 117 a 188 c 151 g 110 t
ORIGIN
Query Match 45.8%; Score 343.8; DB 74; Length 566;
Best Local Similarity 79.2%; Pred. No. 4.9e-87;
Matches 408; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 185 AGGCCTGGAATGATGGGTGAGATCTTACCGGCTCTGGTAGCACCAGAAATACCGAAA 244
Db 51 AGTGGATGGATGGCTCAGTCTTTATGAAGCGGACACAGACAACGCACACTACTCAGACA 110
QY 245 ATTTTAAGACCGGTGTACTATGACGGGTGACACTTCGACTAGTACATATACATGGAGC 304

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|||||
Db 111 GTTTCAGCAGACAGTACCATAACCGCGGACAGTTCACGGCCACAGCCTACATGGAAT 170
QY 305 TCCTCAGCGCTCGGATCGGAGGACACGCGCTCTATTATTGGCGCGTATTATTTTGGTT 364
Db 171 TGAGGACCCCTAAATCTGACGACACGCGCTCTATTATTGTGTGAGAGACCTCCCGTAT 230
QY 365 CTAGCCCGAATTGGTATTATTGATGTTTGGGTCAAGAAACCTCTGCTCACTCTCTCGAGCG 424
Db 231 ATAGTAGTGGCTGCACCTCTCGCATTTGGGCGCAGGAACCTCTCATCTCTCTCTCAG 290
QY 425 CCTCCACAAAGGCGCCATCGGTCTTCCCGCTGGCGCCCTCTCTCCAAGAGCACCTCTGCGG 484
Db 291 CCTCCACAAAGGCGCCATCGGTCTTCCCGCTGGCGCCCTCTCTCCAAGAGCACCTCTGCGG 350
QY 485 GCACAGCGCCCTGGGCTGGCTGCTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCT 544
Db 351 GCACAGCGCCCTGGGCTGGCTGCTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCT 410
QY 545 GGAACCTCAGGCGCCCTGACACAGCGCGTGCACACTTCCCGCTGTCTCCTACAGCTCTCAG 604
Db 411 GGAACCTCAGGCGCCCTGACACAGCGCGTGCACACTTCCCGCTGTCTCCTACAGCTCTCAG 470
QY 605 GACTTACTCTCTCAGCAGCGTGTGACCGTGCCTCTCCAGCAGCTTGGGACCCAGACCT 664
Db 471 GACTTACTCTCTCAGCAGCGTGTGACCGTGCCTCTCCAGCAGCTTGGGACCCAGACCT 530
QY 665 ACATCTGCAAGCTGAATCAAGCCAGCCAGCACACC 699
Db 531 ACATCTGCAAGCTGAATCAAGCCAGCCAGCACACC 565

RESULT 8
LOCUS AW402051 527 bp mRNA EST 16-FEB-2000
DEFINITION UI-HF-BKO-asap-c-05-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3054345 5', mRNA sequence.
ACCESSION AW402051
VERSION AW402051.1 GI:6920737
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
On Feb 24, 1999 this sequence version replaced gi:4058273.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1..527
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3054345"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTI)"
/note="Vector: pMT3-Pac; Site:1: NotI; Site:2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA"

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(0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

Query Match 45.5%; Score 341.2; DB 72; Length 527;
Best Local Similarity 95.1%; Pred. No. 2,7e-86;
Matches 352; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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BASE COUNT      112 a      185 c      133 g      97 t
ORIGIN
      379 TATTGATGTTGGGGTCAAGAACCTGTCTACTGTCTGTGAGCGCTCCACCAAGGCG 438
            || || || || || || || || || || || || || || || || || || || ||
      149 TACATGACGCTGGGGCAAGGACGATCCCGCTCTCTCAGCTCCACCAAGGCG 208
      439 CCATCGGCTTCCCGGGGGGCGCTCTCCAGAGCACTTGGGGGACAGCGGCGCTG 498
            || || || || || || || || || || || || || || || || || || || ||
      209 CCATCGGCTTCCCGGGGGGCGCTCTCCAGAGCACTTGGGGGACAGCGGCGCTG 268
      499 GCGTGGCTGTCAGAGACTACTTCCCGGAACCGGTGACGCTGTGTGGAAGTCAAGCGCC 558
            || || || || || || || || || || || || || || || || || || || ||
      269 GCGTGGCTGTCAGAGACTACTTCCCGGAACCGGTGACGCTGTGTGGAAGTCAAGCGCC 328
      559 CTGACCAAGCGGCGTGCACACCTTCCGGCTGTCTCTACAGTCTCAGAGCTACTCTCC 618
            || || || || || || || || || || || || || || || || || || || ||
      329 CTGACCAAGCGGCGTGCACACCTTCCGGCTGTCTCTACAGTCTCAGAGCTACTCTCC 388
      619 AGAGAGCTGTGTGACGCTGCTCCAGAGCTGTGGGACAGCTTACATGTGCAAGCTG 678
            || || || || || || || || || || || || || || || || || || || ||
      389 AGAGAGCTGTGTGACGCTGCTCCAGAGCTGTGGGACAGCTTACATGTGCAAGCTG 448
      679 AATCACAAGCCGACGACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGACAAA 738
            || || || || || || || || || || || || || || || || || || || ||
      449 AATCACAAGCCGACGACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGACAAA 508
      739 ACTCACAACAT 748
            || || || || || || || || || || || || || || || || || || || ||
      509 ACTCACAACAT 518
      509 ACTCACAACAT 518

RESULT 9
LOCUS      AM177689      442 bp      mRNA      EST      16-NOV-1999
DEFINITION R1-CT0199-100999-021-A07 CT0199 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AM177689
VERSION     AM177689.1 GI:6443726
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 442)
AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
TITLE      The FAPESP/LICR Human Cancer Genome Project
JOURNAL    Unpublished (1999)
COMMENT    On Apr 3, 1998 this sequence version replaced gi:3018868.
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1st2-RC1-CT0199-
            100999-021-A07&tl=1998-09-10&tl=1)
            Seq primer: puc 18 forward
            High quality sequence start: 32
            High quality sequence stop: 442.
            Location/Qualifiers
                1..442
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0199"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site.1: Sma1; Site.2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions." 89 t

BASE COUNT 78 a 123 c 152 g
ORIGIN

```
Query Match 44.7%; Score 335.6; DB 69; Length 442;
Best Local Similarity 96.1%; Pred. No. 9,8e-85;
Matches 344; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

      391 TGGGATCAAGAACCTGTGCTACTGTCTGAGCGCTCCACCAAGGCGCATCGTCTTC 450
            || || || || || || || || || || || || || || || || || || || ||
      401 TGGGATCAAGAACCTGTGCTACTGTCTGCTGCTCAGCTCCACCAAGGCGCATCGTCTTC 342
      451 CCGCTGGGCGCTCTCTCCAGAGCACTTGGGGGACAGCGGCGCTGGCTGTGCTC 510
            || || || || || || || || || || || || || || || || || || || ||
      341 CCGCTGGGCGCTCTCTCCAGAGCACTTGGGGGACAGCGGCGCTGGCTGTGCTC 282
      511 AAGGACTACTTCCCGGAACCGGTGACGCTGTGTGGAAGTCAAGCGGCGCTGACAGCGCG 570
            || || || || || || || || || || || || || || || || || || || ||
      281 AAGGACTACTTCCCGGAACCGGTGACGCTGTGTGGAAGTCAAGCGGCGCTGACAGCGCG 222
      571 GTCGACACTTCCCGGCTGTCTTACAGTCTTACAGTCTTACCTCTGACAGCGGCTG 630
            || || || || || || || || || || || || || || || || || || || ||
      221 GTCGACACTTCCCGGCTGTCTTACAGTCTTACAGTCTTACCTCTGACAGCGGCTG 162
      631 ACCGTGCTCCAGAGCTTGGGACAGCTTACATGTGACAGTGTATACAAAGCC 690
            || || || || || || || || || || || || || || || || || || || ||
      161 ACCGTGCTCCAGAGCTTGGGACAGCTTACATGTGACAGTGTATACAAAGCC 102
      691 AGCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGACAAAACATGACACAT 748
            || || || || || || || || || || || || || || || || || || || ||
      101 AGCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGACAAAACATGACACAT 442
      101 AGCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGACAAAACATGACACAT 442

RESULT 10
LOCUS      AM606367      634 bp      mRNA      EST      23-MAR-2000
DEFINITION OVO-HT0366-280100-088-h06 HT0366 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AM606367
VERSION     AM606367.1 GI:7311108
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 634)
AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
TITLE      The FAPESP/LICR Human Cancer Genome Project
JOURNAL    Unpublished (1999)
COMMENT    On May 7, 1998 this sequence version replaced gi:3118833.
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&tl=2-QV0-HT0366-
            280100-088-h06&tl=2000-01-28&tl=1)
            Seq primer: puc 18 forward
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High quality sequence start: 7
High quality sequence stop: 633.
Location/Qualifiers
1..634
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0366"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 130 a 172 c 193 g 139 t
ORIGIN

Query Match 44.5%; Score 333.6; DB 74; Length 634;
Best Local Similarity 74.2%; Pred. No. 4e-84;
Matches 451; Conservative 0; Mismatches 149; Indels 8; Gaps 2;
QY 95 AGCCAGGGGCTCAGTCAAGTGTCTCTAAGCTAGCGGCTATATTTTCTAATTT 154
Db 609 AGCCCGCAAGTCTCTGAGACTCTCTGTGAAGCCTCTGGAATCAGTTCGACGATTATG 550
QY 155 GGATTCATGGTGGTTCAGGCCCCGGGAGGCGCTGGATGGATGGTGAGATCTTAC 214
Db 549 CCATGCACTGGTGGTCCGGCAAGCTCCAGGAAGGGCGCTGGAGTGGTCTCAGGTATCACTT 490
QY 215 CGGCTCTGGTAGCACCGCAATATACGAAATTTTAAAGACGCTGTACTATGACCGTG 274
Db 489 GGAATAGTGAATGAAGACTATGGGACTCTGTGAAGGGCGGATTCACATCTCCAGAG 430
QY 275 ACATTCGACTAGTACAGTACATACATGAGTCTCCAGGCTCGGATCGGAGGACAGCGCG 334
Db 429 ACACGTCAGAACTCCCTATATCTACAGTTGAACAGTCTGAGATTTGAGACAGCGCT 370
QY 335 TCTATTATGCGCGGTTTATTTTGGTTCTAGCCCGAATGG-----TATTTTATG 388
Db 369 TCTATTACTGCGGAGAGATATCTTGTGGGAGCTACGAGATGGGGAACATGCATTGTATC 310
QY 389 TTTGGGTCAGGAACCTTGTCACCTGTCAGGCGCTCCAGCAAGGCGCCATCGGCT 448
Db 309 TCTGGGCGGAGGACCATATGTCACCGTCTCTACGCTCCAGCAAGGCGCCATCGGCT 250
QY 449 TCCCGCTGGCGCCCTCCCTCAAGAGACACTCTGGGGGACAGCGCGCTCGGCTGCTGG 508
Db 249 TCCAGCTGGCACCTCTCCAGAGACACTCTGGGGGACAGCGCGCTCGGCTGCTGG 190
QY 509 TCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCGCTCGACAGCG 568
Db 189 TCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACCTCAGCGCGCTCGACAGCG 130
QY 569 GCGTGCACACTTCCCGGCTGCTCAGTCTCTAGGACTCTACTCCCTCAGCAGCGTGG 628
Db 129 GCGTGCACACTTCCCGGCTGCTCAGTCTCTAGGACTCTACTCCCTCAGCAGCGTGG 70
QY 629 TGACCGTCCCTCCAGAGCTTGGGCACCCAGACCTACATCTGCAACGTTGAATCAACAAC 688
Db 69 TGACCGTCCCTCCAGAGCTTGGGCACCCAGACCTACATCTGCAACGTTGAATCAACAAC 12
QY 689 CCAGCAAC 696
Db 11 CAACAACC 4

RESULT 11
AW606325
LOCUS
DEFINITION QV0-HT0366-280100-088-509_1 HT0366 Homo sapiens cDNA, mRNA
sequence.
455 bp mRNA EST 23-MAR-2000

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW606325.1 GI:7311066
EST.
human.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 455)
HCGP <http://www.ludwig.org.br/ORESTES>.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
On May 7, 1998 this sequence version replaced gi:3118791.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ci=QV0&t2=QV0-HT0366-280100-088-b09_1&t3=2000-01-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 455.
Location/Qualifiers
1..455
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0366"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 94 a 155 c 116 g 90 t
ORIGIN

Query Match
Best Local Similarity
Matches 362; Conservative 0; Mismatches 36; Indels 1; Gaps 1;

QY 351 TTATTTTGGTCTAGCCGGAATTTGTTATTTGATTTTGGGTCAAGGAACCTGGT 410
Db 11 TTATTTGCTCTGGTGGTCCCTGCTCTGATATCTGGGGCCAGGGACAATGGT 70
QY 411 CACTGTCTCAGCGCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCGCTCTCCCAA 470
Db 71 CAACGTCTTTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCGCTCTCCAG 130
QY 471 GAGCACCTCTGGGGGACAGCGCCCTGGCTGCTTGGTCAAGGACTACTTCCCGAACC 530
Db 131 GAGCACCTCCGAGAGACAGCGCCCTGGCTGCTTGGTCAAGGACTACTTCCCGAACC 190
QY 531 GGTGACGGTGTCTGTGAACCTCAGCGCCCTGACACAGCGGCTGCACACCTTCCCGGCTGT 590
Db 191 GGTGACGGTGTCTGTGAACCTCAGCGCTCTGACAGGGGCTGCACACCTTCCCGGCTGT 250
QY 591 CCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCGTCCCTCCAGCAGCTT 650
Db 251 CCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCGTCCCTCCAGCAGCTT 310
QY 651 GGGCACCCAGACCTACATCTGCAACGTGAATCAC -RAGCCCCACACACCAAGTGGACA 709
Db 311 GGGCACCCAGACCTACATCTGCAACGTGAATCACAAAGCCCAACACCAAGTGGACA 370
QY 710 AGAAAGTTGAGCCCAAAATCTTGTGACAAAACTCACACAT 748
Db 11

Db 371 AGAGAGTTGAGCCCAATCTTGACAAAACACTCACACAT 409

RESULT 12
AM403670
LOCUS AM403670 579 bp mRNA EST 16-FEB-2000
DEFINITION UI-HF-BK0-abh-b-03-0-01.f1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056189 5', mRNA sequence.
ACCESSION AM403670
VERSION AM403670.1 GI:6922678
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
1 (bases 1 to 579)
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/INL at:
www.bio.lnl.gov/db/ftp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1. 579
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_line="geminal center B cells"
/lab_host="DH10B (LTI)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafio, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 121 a 207 c 150 g 101 t

ORIGIN

Query Match 42.9%; Score 322; DB 72; Length 579;
Best Local Similarity 81.7%; Pred. NO. 7.5e-81;
Matches 405; Conservative 0; Mismatches 70; Indels 21; Gaps 2;

274 GACACTGCGACTAGTATACATAGATGAGGCTCCGCGCCGATCGAGACAGCC 333
10 GAAAGGCCCAACACACCGCTACCTGCAAGGAGCCCTCGGACCCGCC 69
334 GGTATATATGCGCGCTATTTTGTGTCTAGCCGGAAT-----TGG 378
70 ATGTATTACGTGCGAGACATGGGTTCCAGATGTAGTACCACTGCTATGGGTG 129
379 TATTGTGATGTTGGGGTCAAGAACCTGTGCTACGTCTGAGCGCCTCCACCAAGGC 438
130 TGGTTCGACCCCTGGGGCGAGGAACCTGTGCTACCGTCTCCTGAGCTTCACCAAGGC 189
439 CCATCGGCTCTTCCCTGGGGCCCTCTCCCAAGACACCTTGGGGGACAGCGCCCTG 498
190 CCATCGGCTCTTCCCTGGGGCCCTCTCCCAAGACACCTTGGGGGACAGCGCCCTG 249
499 GGGTGGCTGGTCAAGAGCTCTTCCCGAACCAGTGGAGCGGTGTGAACCTAGCGGCC 558
250 GGCTGGCTGGTCAAGAGCTCTTCCCGAACCAGTGGAGCGGTGTGAACCTAGCGGCC 309

559 CTGACACAGCGGCTGACACACCTTCCCGGCTGTCTACAGTCTCAGAGACTTACTCCCTC 618
310 CTGACACAGCGGCTGACACACCTTCCCGGCTGTCTACAGTCTCAGAGACTTACTCCCTC 369
619 AGCAGCGTGTGACCGCTGCTCCAGACAGCTTGGGACCCAGACCTTACATCTGCAACGTG 678
370 AGCAGCGTGTGACCGCTGCTCCAGACAGCTTGGGACCCAGACCTTACATCTGCAACGTG 429
679 AATCACAAGCCCAAGCAACACCAAGTGGAGCAAGAAAGTTGAGCCCAATC-----TTGT 732
430 AATCACAAGCCCAAGCAACACCAAGTGGAGCAAGAAAGTTGAGCTCAAAACCCCACTTGT 489
733 GACAAACTCACACAT 748
490 GACAAACTCACACAT 505

RESULT 13
AM375944/c
LOCUS AM375944 442 bp mRNA EST 04-FEB-2000
DEFINITION RC0-CT0201-270999-011-e04 CT0201 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM375944
VERSION AM375944.1 GI:6880598
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE HCGP <http://www.ludwig.org.br/ORESTES>.
1 (bases 1 to 442)
THE PAPESP/LICR HUMAN CANCER GENOME PROJECT
JOURNAL Unpublished (1999)
COMMENT On Jul 8, 1999 this sequence version replaced gi:5422592.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC2&t2=RC0-CT0201-270999-011-e04&t3=1999-09-27&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 442.
Location/Qualifiers
1. 442
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0201"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 78 a 106 c 166 g 92 t

ORIGIN

Query Match 42.8%; Score 320.8; DB 71; Length 442;
Best Local Similarity 99.4%; Pred. NO. 1.5e-80;
Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

435 CCTCACCAAGGCGCCATCGCTTCCCTGGCGCCCTCTCCCAAGACACTCTGGGG 484
442 CCTCACCAAGGCGCCATCGCTTCCCTGGCGCCCTCTCCCAAGACACTCTGGGG 383

BASE COUNT 92 a 160 c 118 g 76 t
ORIGIN

Query Match 42.5%; Score 318.6; DB 72; Length 446;
Best Local Similarity 88.3%; Pred.No. 6.5e-80;
Matches 361; Conservative 0; Mismatches 39; Indels 9; Gaps 1;

QY 320 CGGAGACACGGCGCTATTATTGGCGCTTATTTTTTGGTTCTAGCCCGAATTGGT 379
Db 8 CTGACACACGGCGCTATTATTGCGAGAGAGTCCAGTGGCTGGCC----- 58

QY 380 ATTTGATCTTTGGGTCAAGGAACCTTGGTCACTGTCTCGAGCGCTCCACCAAGGGCC 439
Db 59 ACCATGACTACTTGGGCCAGGGAACCTTGGTCACTGTCTCGAGCTTCCACCAAGGGCC 118

QY 440 CATCGGTCTTCCCGTGGCGCCCTCTCCAAAGACACCTCTGGGGGCACAGGGCCCTGG 499
Db 119 CATCGGTCTTCCCGTGGCGCCCTCTCCAGGAGCACCTCTGGGGGCACAGGGCCCTGG 178

QY 500 GCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC 559
Db 179 GCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCC 238

QY 560 TGACGAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCCTCAGGACTCTTACTCCCTCA 619
Db 239 TGACGAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCCTCAGGACTCTTACTCCCTCA 298

QY 620 GCAGGCTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAGTGA 679
Db 299 GCATGCTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAGTGA 358

QY 680 ATCAAGCCCCAGCACACCAAGGTGGACAAGAAAGTTGAGCCCAATC 728
Db 359 ATCAAGCCCCAGCACACCAAGGTGGACAAGAAAGTTGAGCTCAAAAC 407

Search completed: September 12, 2000, 20:04:56
Job time: 3493 sec

Db 61 GTCCACTGGTCAATCCGGCGCCGAGSTCAAGACCAGGGCCCTCAGTCAAGTGTCC 120

Best Local Similarity 81.5%; Pred. NO. 7.7e-114;
Matches 585; Conservative 0; Mismatches 130; Indels 3; Gaps 1

QY	1	ATGAAGTGGACCTGGGATATCTCTTCCCTCCCTGACATTAACCTGGCCGCGACCTCCCA	60
Db	21	ATGGGATGGACCTGTATCATCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCTCA	80
QY	61	GTCCAACTGTGTGCAATCCGGCGGAGGTCAAGAACGACAGGGGCTTCAGTCAAAAGTCC	120
QY	81	GTCACAGCTGGTCAAGTCTGGGGGCTGAGGTCAAGAACGCTTGGGCTTCAGTAAGAGTCC	140
Db	121	TGTAAAGTACGGGCTATATTTTCTTAATTTATTTGGATTCAAATGGGTGGCTCAGGCCCC	180
Db	141	TGCAGGCTTGTGGCTACACCTTACACAGCTACGATGAGTGGGTAACAGAGGCCCT	200
QY	181	GGGAGGGGCTGGATGGATGGGTGGAATCTTACCGGGCTCTGGTAGCAGCGAATATAC	240
Db	201	GGACAGGGGCTTGAATGGATGGAGAGATTTGATTCCTCTGTATAGCTATTAATCAAT	260
QY	241	GAAATTTTAAAGACCGGTACTATGATACGGGTGACACTTGCATAGTACAGTATACATG	300
Db	261	CAAAAGTCAAGGGCAAGGGCCATTTACATGTATAGACATCCATCAGTACACAGCTCATG	320
QY	301	GAGCTCTCCACCCGCAATGCGAGACACGGCCCTGATATATTTGCGGGCTATTTT	360
Db	321	GAGCTCAGACGCTGAGATCTGAGAGACACGGGCTCTATTAATCTGTGCAAGAA--TAGG	377
QY	361	GTTTCTACGCCGAATTTGGTATTTTGGATGTTGGGTCAAGAAACCGTGCTACTGTCTG	420
Db	378	GACTATAGTAACTAGTACTTGTGATGTCTGGGGCGAAGGAGACCTGGTACACGCTCC	437
QY	421	AGCCGCTCCACCAAGGGCCCATCGGTCTTCCCTGGCGCCCTCTCTCAAGACACCTCT	480
Db	438	TCAAGCTTCACCAAGGGGCCATCGGTCTTCCCTGGCACCTCTCTCAAGACACCTCT	497
QY	481	GGGGGACAGGGGCGCTGGGCTGGTCTGAAGGACACTTCCCGCAACCGGTGAGCGTG	540
Db	498	GGGGGACAGGGGCGCTGGGCTGGTCTGAAGGACACTTCCCGCAACCGGTGAGCGTG	557
QY	541	TCTGTGAACCTCAGGCGGCGCTTACGAGGGGGGTGACACACTTCCCGGCTGTCTACAGTCC	600
Db	558	TCTGTGAACCTCAGGCGGCGCTTACGAGGGGGGTGACACACTTCCCGGCTGTCTACAGTCC	617
QY	601	TCAGACTCTACTCCCTCAGCAGCGTGTGATCGCTGCCCTCCAGCAGCTTGGGCACCCAG	660
Db	618	TCAGACTCTACTCCCTCAGCAGCGTGTGTACCGCTGCCCTCCAGCAGCTTGGGCACCCAG	677
QY	661	ACCTACATCTCCCAAGTGAATCAACAACCCAGCAACCCAAAGGTGACAAAGAAAGTTG	718
Db	678	ACCTACATCTCCCAAGTGAATCAACAACCCAGCAACCCAAAGGTGACAAAGAAAGTTG	735
RESULT	6		
ID	V44956		
AC	V44956	standard; cDNA; 8120 BP.	
DT	15-FEB-1999	(first entry)	
DE	Anti-IL-8 humanised antibody plasmid p6G4V11N35A.chosD.9.	a	
KW	Humanised antibody; chimeric antibody; monoclonal antibody; mouse;		
KW	human; Fcb; interleukin-8; inflammation; immunotherapy; psoriasis;		
KW	inflammatory bowel disease; Crohn's disease; ulcerative colitis;		
KW	ischemic reperfusion; adult respiratory distress syndrome;		
KW	dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;		
KW	rheumatoid arthritis; Sjogren's syndrome; vasculitis;		
KW	leukocyte diapedesis; multiple organ injury syndrome; septicemia;		
KW	trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;		
KW	vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;		
KW	therapy; p6G4V11N35A.chosD.9; ds; cyclic; circular.		
OS	Chimeric - Mus sp.		
OS	Chimeric - Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	CDS	1363..2721	
FT		/*tag- a	

MO837200-A2.
 27-AUG-1998.
 PF 20-FEB-1998; U03337,
 PR 22-JAN-1998; US-012116.
 PA 21-FEB-1997; US-804444.
 (GETH) GENENTECH INC.
 Hsai V, Kouments I, Leong SR, Presta LR, Shahrokh Z,
 Zapata GA:
 WPI: 98-467563/40.
 P-PSDB: W69316.
 New conjugates of antibody fragments - having covalently attached
 non-proteinaceous polymer molecules, particularly polyethylene
 glycol, for improving the residence time in the circulation.
 PS Example P: Fig 48A-Z: 328pp. English.
 CC This is the DNA sequence of vector plasmid p6C4V11N35A.chosd.9
 encoding a humanised 6C4V11N35A IgG (see W69316) containing
 complementarily determining regions of murine anti-interleukin-8
 (IL-8) monoclonal antibody (Mab) 6G5.2.5 (see W69309-10) in a
 human template. The plasmid has a pSV1 backbone. Humanised
 anti-IL-8 MAb (see W69301-04) are described for use in diagnostic
 applications and in the treatment of inflammatory disorders. The
 invention provides conjugates of an antibody fragment and a
 polymer, such as PEG, that have improved half-life, mean residence
 time, and/or clearance rate. The conjugates can be used for immune
 therapy of e.g. psoriasis, responses associated with inflammatory
 bowel disease (such as Crohn's disease and ulcerative colitis),
 ischemic reperfusion, adult respiratory distress syndrome,
 dermatitis, meningitis, encephalitis, uveitis, autoimmune diseases
 such as rheumatoid arthritis, Sjorgen's syndrome, vasculitis,
 diseases involving leukocyte diapedesis, central nervous system
 inflammatory disorder, multiple organ injury syndrome secondary to
 septicæmia or trauma, alcoholic hepatitis, bacterial pneumonia,
 antigen-antibody complex mediated diseases, inflammations of the
 lung, including pleurisy, eosinophilia, vasculitis, pneumonia,
 chronic bronchitis, bronchiectasis, and cystic fibrosis.
 Sequence 8120 BP: 2023 A: 2182 C: 1958 G: 1957 T:

Query Match	Score	DB 1	Length
65.48;	490.4;	DB 1;	8120;

Matches 587; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

[illegible]

QY 481 GGGGGCAGCGGCGCTGGCTGCTGCTGAAGGACTACTTCCCGAACCAGGTGACGGTG 540
 DB 1786 GGGGGCAGCGGCGCTGGCTGCTGCTGAAGGACTACTTCCCGAACCAGGTGACGGTG 1845
 QY 541 TCGTGGAACTCAGCGGCGCTGACGAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCC 600
 DB 1846 TCGTGGAACTCAGCGGCGCTGACGAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCC 1905
 QY 601 TCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGTGTGGGACCCAG 560
 DB 1906 TCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGTGTGGGACCCAG 1965
 QY 661 ACCTACATCTCAACGCTGAATCAAGCCAGCAACAGGTGGCAAGAAAGTTGAG 720
 DB 1966 ACCTACATCTCAACGCTGAATCAAGCCAGCAACAGGTGGCAAGAAAGTTGAG 2025
 QY 721 CCCAAATCTTGACAAAACCTACACAT 748
 DB 2026 CCCAAATCTTGACAAAACCTACACAT 2053

RESULT 7

V70079
 ID V70079 standard; DNA; 2077 BP.
 AC V70079;
 DE Anti-Fas humanised antibody HFE7A heavy chain DNA.
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; ds.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 CDS 27..2042
 FT FT /*tag= a
 FT FT /note= "contains introns"
 FT FT 28..83
 FT FT /*tag= b
 FT FT 1..741
 FT FT /*tag= c
 FT FT /number= 1
 FT FT /codon_start= 27
 FT FT 742..1132
 FT FT /*tag= d
 FT FT /number= 1
 FT FT 1133..1177
 FT FT /*tag= e
 FT FT /number= 2
 FT FT 1178..1295
 FT FT /*tag= f
 FT FT /number= 2
 FT FT 1296..1625
 FT FT /*tag= g
 FT FT /number= 3
 FT FT 1626..1722
 FT FT /*tag= h
 FT FT /number= 3
 FT FT 1723..2077
 FT FT /*tag= i
 FT FT /number= 4
 PN AU9859701-A.
 PD 08-OCT-1998.
 PF 30-MAR-1998; 059701.
 PR 08-OCT-1997; JP-276064.

PR 01-APR-1997; JP-082953.
 PR 25-JUN-1997; JP-169088.
 PA (SANY) SANKYO CO LTD.
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I,
 PI Masahiko O, Nobutsu S, Shin Y, Tohru T;
 DR WPI: 98-543440/47.
 DR P-PSDB: W83036.
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 PS Claim 27; Page 210-212; 292pp; English.
 CC This nucleotide sequence codes for the VD type humanised heavy
 CC chain (see W83036) of murine anti-human Fas monoclonal antibody
 CC PCR amplification of human genomic DNA. Host cell Escherichia coli
 CC pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion
 CC fragment of the humanised VD type HFE7A heavy chain and DNA
 CC encoding human IGH1 constant region, and is deposited as
 CC FERM BP-6074 (claimed). The invention provides methods for
 CC producing humanised antibodies by culturing host cells. Humanised
 CC versions of HFE7A (see W83031-37), like native HFE7A, are capable
 CC of inducing apoptosis in abnormal cells expressing Fas, and of
 CC inhibiting Fas-induced apoptosis in normal cells. The humanised
 CC antibodies are used to evaluate, in animal models, treatments of
 CC diseases that involve Fas/Fas ligand interactions, and also to
 CC treat such diseases, including autoimmune disease (e.g. systemic
 CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
 CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
 CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
 CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 SQ Sequence 2077 BP; 461 A; 685 C; 566 G; 365 T;
 Query Match 65.2%; Score 489.2; DB 1; Length 2077;
 Best Local Similarity 81.1%; Pred. No. 1.2e-112;
 Matches 582; Conservative 0; Mismatches 133; Indels 3; Gaps 1;
 QY 1 ATGAAGTGGAGCTGGGTATTCTCTCTCTCTAGTAACTGCCGGCGCTCCACTCCCAA 60
 DB 27 ATGGGATGGAGCTGTATCATCTCTCTCTGGTAGCAGCAGCTACAGGTCTCACTCTAG 86
 QY 61 GTCCAACTGGTGCAATCCGGCGCCGAGAGTCAAGAACCCAGGGCGCTCAGTCAAGTGTCC 120
 DB 87 GTCCAACTGGTGCACTCTGGGGCTGAGGTCAAGAGCCCTGGGGCTTCACTGAGGTGTCC 146
 QY 121 TGTAAAGCTAGCGGCTATATTTTCTTAATATTTGATTCAATGGGTGGGTGAGGCCCCC 180
 DB 147 TGCAGGGCTTCTGGCTACACCTTCCACAGCTACTGGATGCAGTGGGTAAACAGGCCCT 206
 QY 181 GGCAGGGGCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCAGCCGATATACC 240
 DB 207 GGACAGAGGCTTGGTGGATGGGAGAGATTGATCTTCTGTAGCTATATACTACATAAT 266
 QY 241 GAAATTTTAAAGACCGTGTATTACTATGACCGCTGACACTTCGACTAGTACAGTATACATG 300
 DB 267 CAATAGTTCAAGGCAAGCCACATTGACTGTAGACACATCCGCTAGCAGCCATACATG 326
 QY 301 GAGCTCTCCAGCCTCGGATCGGAGGACACGGCGTCTATTATTGCGCGGCTTATTTTTTT 360
 DB 327 GAGCTCAGCAGCCTGAGATCTGAGGACACGGCGGTCTATTACTGTGCAAGAAA---TAGG 383
 QY 361 GGTCTAGCCCGAATTTGGTATTTTGGTGTTCAGGACACCCCTGGTCACTGTCTCG 420
 DB 384 GACTATAGTAACAACACTGGTACTTCGAGTGTGGGGGCAAGGGACCCCTGGTCTCC 443
 QY 421 AGCGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCGCCCTCCCTCCCAAGAGCAGCTCT 480
 DB 444 TCAGGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTCTCTCCCAAGAGCAGCTCT 503

QY 481 GGGGACAGCGCCCTGGCTGCTGCTCAAGACTACTTCCCGACCCGGTGACGTTG 540
 DB 504 GGGGACAGCGCCCTGGCTGCTGCTGCTCAAGACTACTTCCCGACCCGGTGACGTTG 563
 QY 541 TCGTGAGACTACGCGCCCTGACAGCGCGCTGACACACTTCCCGCTCTCCACAGTCC 600
 DB 564 TCGTGAGACTACGCGCCCTGACAGCGCGCTGACACACTTCCCGCTCTCCACAGTCC 623
 QY 601 TCAGGACTCTACTCCCTGACAGCGCTGACAGCGCTGCTCCAGAGCTTGGCACCAG 660
 DB 624 TCAGGACTCTACTCCCTGACAGCGCTGACAGCGCTGCTCCAGAGCTTGGCACCAG 683
 QY 661 ACTTACATCTGCAACGTGATCAAGACCCAGCAACACCAAGGTGACAGAAAGTTG 718
 DB 684 ACTTACATCTGCAACGTGATCAAGACCCAGCAACACCAAGGTGACAGAAAGTTG 741

RESULT 8
 V55073
 ID V55073 standard; DNA; 801 BP.
 AC V55073:
 DT 15-FEB-1999 (first entry)
 DE Humanised anti-IL-8 6G4.2.SV11N35A Fab heavy chain DNA.
 KW Humanised antibody; monoclonal antibody; Fab; interleukin-8;
 KW 6G4.2.5; inflammation; immunotherapy; therapy; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW ischaemic reperfusion; adult respiratory distress syndrome;
 KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
 KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
 KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;
 KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
 KW vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
 KW ds
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 OS Synthetic.
 FH Key Location/Qualifiers
 OS CDS 31..801
 FT sig_peptide /tag- a
 FT 31..99
 FT /note= "Still peptide leader"
 FT mat_peptide 100..798
 FT /tag- C
 PN W09837200-A2.
 PD 27-AUG-1998.
 PF 20-FEB-1998; U03337.
 PR 22-JAN-1998; US-012116.
 PR 21-FEB-1997; US-804444.
 PA (GETH) GENENTECH INC.
 PI Hsai V, Koumenis I, Leong SR, Presta LR, Shahrokh Z,
 PI Zapata GA.
 DR WPI: 98-467563/40.
 DR P-SDS: W69304.
 PT New conjugates of antibody fragments - having covalently attached
 PT non-proteinaceous polymer molecules, particularly polyethylene
 PT glycol, for improving the residence time in the circulation.
 PS Example 1: Fig 53; 328pp; English.
 CC This DNA sequence encodes humanised anti-interleukin-8 (IL-8)
 CC antibody 6G4.2.SV11N35A Fab' heavy chain (see W69304) modified to
 CC contain a Cys residue in the hinge region, and which contains the
 CC complementarily determining regions (CDRs) of murine anti-IL-8
 CC antibody 6G4.2.5 heavy chain within a human IgG1 subgroup III heavy
 CC (Mabs) and variants are described for use in diagnostic applications
 CC and in the treatment of inflammatory disorders. The invention
 CC provides conjugates of an antibody fragment and a non-proteinaceous
 CC polymer, such as PEG, that have improved half-life, mean residence
 CC time, and/or clearance rate compared to non-derivatised parental
 CC antibody fragment. Also claimed is a Fab' or Fab-SH antibody
 CC fragment comprising a heavy chain amino acid sequence composed of
 CC amino acids +1-233 of the heavy chain polypeptide of 6G4.2.SV11N35A

CC Fab'. The conjugates are used for immune therapy of inflammatory
 CC disorders, e.g. psoriasis, responses associated with inflammatory
 CC bowel disease (such as Crohn's disease and ulcerative colitis),
 CC ischemic reperfusion, adult respiratory distress syndrome,
 CC dermatitis, meningitis, encephalitis, uveitis, autoimmune diseases
 CC such as rheumatoid arthritis, Sjorgen's syndrome, vasculitis,
 CC diseases involving leukocyte diapedesis, central nervous system
 CC inflammatory disorder, multiple organ injury syndrome secondary to
 CC septicemia or trauma, alcoholic hepatitis, bacterial pneumonia,
 CC antigen-antibody complex mediated diseases, inflammations of the
 CC lung, including pleurisy, alveolitis, vasculitis, pneumonia,
 CC chronic bronchitis, bronchiectasis, and cystic fibrosis. They can
 CC also be used in diagnostic applications.
 SQ Sequence 801 BP; 176 A; 235 C; 204 G; 186 T;

Query Match 65.1%; Score 488; DB 1; Length 801;
 Best Local Similarity 79.4%; Pred. No. 1.9e-112;
 Matches 578; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 21 TCTCTCCCTCCCTGCACTAGTACGCGCGCTCCACCTCCAGTCCAACTGGTGCATCCG 80
 DB 63 TATGTTCTGTTTCTTCTATTCTCTACAAAGCGCTGAGCTTCAAGTGCAGTCTGG 122
 QY 81 CGCCGAGGTCACAGAGCAGGAGCGCTCAGTCAAAAGTGTCTCTAAAGCTAGCGCTATAT 140
 DB 123 CGGTGGCTGTGTGACGACAGGAGGCTACCTCCGTTTCTCTGTGACCTTCTGGTACTC 182
 QY 141 TTTTCTAATTATTTGATTCATATGCTGCTGCTGACGCCCCGCGAGGCGCTGGAATGAT 200
 DB 183 CTCTCGAGTCACTATATGACATGCGGCTCAGGCCCCGGGTAAAGGCGCTGGAATGAT 242
 QY 201 GGGTGAATTTTACCGGCTCTGTGACACCAATATACGAAATTTTAAACCGCTG 260
 DB 243 TGGATATATGATGCTTCCATATGTGAATACCTAGTATATCAAAAGTTCAAGGCGCTTT 302
 QY 261 TACTATGACGCTGACACTCTGACTAGTATACATGATGAGCTCCAGCGCTGATC 320
 DB 303 CACTTTATCTCGGACACTCCAAAACACAGCATCTCTCAATGAAAGCTTCTGCTGC 362
 QY 321 GGAAGACAGCGCGCTGATTTATTTGCGCGCTTATTTTGGTTCTAGCCGATTTGTA 380
 DB 363 TGAAGACACTGCGCTGATTTAGTGTGCAAGAGGAGATATCGTACAAATGATGCTG 422
 QY 381 TTTTGTATTTTGGGCTCAAGAAACCTGTGCTACTGTCTGACGCGCTCCACAAAGGCC 440
 DB 423 CTTCGAGCTCTGGGGTCAAGAAACCTGTGCTACCGCTCTCCGCGCTCCACAAAGGCC 482
 QY 441 ATGAGTCTTCCCGCTGGCGCTCTCTCAAGAGACCTCTGGGGGACAGCGCGCTGGG 500
 DB 483 ATGAGTCTTCCCGCTGGCGCTCTCTCAAGAGACCTCTGGGGGACAGCGCGCTGGG 542
 QY 501 CTGCTGTGTCAGAGACTACTTCCCGAACCAGGCTGACGCTGTGTAAGTCAAGCGCCT 560
 DB 543 CTGCTGTGTCAGAGACTACTTCCCGAACCAGGCTGACGCTGTGTAAGTCAAGCGCCT 602
 QY 561 GACCAGGCGCTGACACCTTCCCGGCTGTCTTCAAGTCTCTCAAGAGTCTTCTCTCAG 620
 DB 603 GACCAGGCGCTGACACCTTCCCGGCTGTCTTCAAGTCTCTCTCAAGAGTCTTCTCTCAG 662
 QY 621 CACGCTGTGACGCTGCTCCAGACCTTGGGACACCAAGTCTTCAAGTCTTCTCTCAG 680
 DB 663 CACGCTGTGACGCTGCTCCAGACCTTGGGACACCAAGTCTTCAAGTCTTCTCTCAG 722
 QY 681 TCACAGCCGAGCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGCAAAAC 740
 DB 723 TCACAGCCGAGCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGCAAAAC 782
 QY 741 TCACACAT 748
 DB 783 TCACACAT 790

RESULT 9

V55072 standard; DNA; 927 BP.
 AC V55072;
 DT 15-FEB-1999 (first entry)
 DE Humanised anti-IL-8 6G4.2.5V11N35A heavy chain DNA.
 KW Humanised antibody; monoclonal antibody; interleukin-8;
 KW 6G4.2.5; inflammation; immunotherapy; therapy; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW ischaemic reperfusion; adult respiratory distress syndrome;
 KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
 KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
 KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;
 KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
 KW vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
 ds.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 OS Synthetic.
 FH Key Location/Qualifiers
 CDS 31..927
 FT sig_peptide 31..99
 FT /*tag= a
 FT /*tag= b
 FT /*note= "STII peptide leader"
 FT mat_peptide 100..924
 FT /*tag= c
 PN WO9837200-A2.
 PD 27-AUG-1998.
 PF 20-FEB-1998; U03337.
 PR 22-JAN-1998; US-012116.
 PR 21-FEB-1997; US-80444.
 PA (GETH) GENENTECH INC.
 PI Hsai V, Koumenis I, Leong SR, Presta LR, Shahrokh Z,
 PI Zapata GA;
 DR WPI; 98-467563/40.
 DR P-PSDB; W69303.
 PT New conjugates of antibody fragments - having covalently attached
 PT non-proteinaceous polymer molecules, particularly polyethylene
 PT glycol, for improving the residence time in the circulation.
 PS Disclosure; Fig 37; 32pp; English.
 CC This DNA sequence encodes humanised anti-interleukin-8 (IL-8)
 CC antibody 6G4.2.5V11N35A heavy chain (see W69303) in an N-terminal
 CC fusion with the STII leader peptide and in a C-terminal fusion
 CC with the GCN4 leucine zipper, and which contains the complementarity
 CC determining regions (CDRs) of murine anti-IL-8 antibody 6G4.2.5
 CC heavy chain (see W69310) within a human IgG1 subgroup III heavy
 CC chain template. Humanised anti-IL-8 monoclonal antibodies (MABs)
 CC and variants are described for use in diagnostic applications
 CC and in the treatment of inflammatory disorders. The invention
 CC provides conjugates of an antibody fragment and a non-proteinaceous
 CC polymer, such as PEG, that have improved half-life, mean residence
 CC time, and/or clearance rate compared to non-derivatised parental
 CC antibody fragment. Also claimed are a polypeptide that is an
 CC anti-IL-8 MAB or antibody fragment comprising a light chain amino
 CC acid sequence comprising the light chain CDRs of 6G4.2.5V11N35A (see
 CC W69301) or 6G4V11N35E (see W69302) and the heavy chain and leucine
 CC zipper of 6G4.2.5V11N35A, and a F(ab')2 antibody fragment comprising
 CC the heavy chain of 6G4.2.5V11N35A in which the Cys231 and Cys234
 CC residues form a disulphide linkage. The conjugates are used for
 CC immune therapy of inflammatory disorders, e.g. psoriasis, responses
 CC associated with inflammatory bowel disease (such as Crohn's disease
 CC and ulcerative colitis), ischemic reperfusion, adult respiratory
 CC distress syndrome, dermatitis, meningitis, encephalitis, uveitis,
 CC autoimmune diseases such as rheumatoid arthritis, Sjorgen's
 CC syndrome, vasculitis, diseases involving leukocyte diapedesis,
 CC central nervous system inflammatory disorder, multiple organ injury
 CC syndrome secondary to septicemia or trauma, alcoholic hepatitis,
 CC bacterial pneumonia, antigen-antibody complex mediated diseases,
 CC inflammations of the lung, including pleurisy, alveolitis,
 CC vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and
 CC cystic fibrosis. They can also be used in diagnostic applications.
 CC Sequence 927 BP; 217 A; 268 C; 239 G; 203 T;

Query Match 65.1%; Score 488; DB 1; Length 927;
 Best Local Similarity 79.4%; Pred. No. 1.9e-112;
 Matches 578; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 21 TCTCTTCCTCTAGTAACTGCGCGCTCCACTCCCAAGTCCAACTGGTGCATCCGG 80
 DB 63 TATGTTTCGTTTTTCTATTGCTACAAACGCGTACGCTGAGGTTTCAGCTAGTGCAGTCTGG 122
 QY 81 CGCGAGGTCAGAAGCCAGGCGCTCAGTCAAAAGTGTCTGTAAAGCTAGCGGCTATAT 140
 DB 123 CGGTGGCCTGGTGACAGCGGGGCTCACTCCGTTTTTCTGTGTGACGCTTCTGCTACTC 182
 QY 141 TTTTCTTAATATTGATTCAAATGGGTGCGTCAAGGCCCGCGGCGAGGCTGGAATGGAT 200
 DB 183 CTCTCGAGTCACTATATGAGTGGGTGCGTCAAGGCCCGGGTAAAGGCTGGAATGGGT 242
 QY 201 GGTGAGATCTTACCGGGCTCTGTAGCAGCGGAATATACCGAAATTTTAAAGACCGTGT 260
 DB 243 TGGATATATTGATCTTCAATGTTGAACTACGTATATCAAAAGTTCAAAGGCGCTTT 302
 QY 261 TACTATGACGGTGACACTTCGACTAGTACAGTATACATGAGAGCTCTCCAGCCTCGGATC 320
 DB 303 CACTTTATCTCGCGACAACTCCAAAACACAGCATACCTGCAGATGAACAGCCTGCGTGC 362
 QY 321 GGAGGACAGCGCGCTCTATTATTGCGCGGTTATTTTGTGTTCTAGCCCGGAATGGTA 380
 DB 363 TGAGGACACTGCGGCTCTATTACTGTCAAGAGGGGATTATCGCTACAAAGTGGTACTGGTT 422
 QY 381 TTTTGATGTTGGGTCAAGGAACCTTGCTGCTGAGCGCTCCACCAAGGGCCCC 440
 DB 423 CTTCGAGCTCTGGGTCAAGGAACCTTGCTGCTGAGCGCTCCACCAAGGGCCCC 482
 QY 441 ATCGGTCTTCCCGCTGGCGCTCTCTCCAAAGAGCAGCTCTGGGGGACAGCGGCCCTGGG 500
 DB 483 ATCGGTCTTCCCGCTGGCGCTCTCTCCAAAGAGCAGCTCTGGGGGACAGCGGCCCTGGG 542
 QY 501 CTGCTGGTCAAGGACTACTTCCCGAACCGGTGAGCGGTGCTGTGAACTCAGCGGCCCT 560
 DB 543 CTGCTGGTCAAGGACTACTTCCCGAACCGGTGAGCGGTGCTGTGAACTCAGCGGCCCT 602
 QY 561 GACACGCGGTGCACACCTTCCCGGTGCTGTGCTGAGTCTCTAGGACTCTACTTCCCTCAG 620
 DB 503 GACACGCGGTGCACACCTTCCCGGTGCTGTGCTGAGTCTCTAGGACTCTACTTCCCTCAG 662
 QY 621 CAGCGTGGTACCGTCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGA 680
 DB 663 CAGCGTGGTACCGTCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGA 722
 QY 681 TCACAGCCCGACACCAAGGTGGACAGAAAGTTGAGCCCAATCTTGTGACAAAC 740
 DB 723 TCACAGCCCGACACCAAGGTGGACAGAAAGTTGAGCCCAATCTTGTGACAAAC 782
 QY 741 TCACACAT 748
 DB 783 TCACACAT 790

RESULT 10
 V44953

ID V44953 standard; cDNA; 6563 BP.
 AC V44953;
 DT 15-FEB-1999 (first entry)
 DE Anti-IL-8 humanised antibody plasmid p6G4V11N35A.F(ab')2.
 KW Humanised antibody; chimeric antibody; monoclonal antibody; mouse;
 KW human; Fab; interleukin-8; inflammation; immunotherapy; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW ischaemic reperfusion; adult respiratory distress syndrome;
 KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
 KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
 KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;
 KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;

KM vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
 OS therapy; p6g4v1ln35a.f(ab')2; ds.
 KM Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 439..1167
 FT /tag= a
 PN W09837200-A2.
 PD 27-AUG-1998.
 PE 20-FEB-1998; 003337.
 PR 22-JAN-1998; US-012116.
 PR 21-FEB-1997; US-804444.
 PA (GENE) GENENTECH INC.
 PI Hsai V, Kouments I, Leong SR, Presta LR, Shahrokh Z,
 PI Zapata GA;
 DR WPI: 98-467563/40.
 P-PSDB: W69313.
 PT New conjugates of antibody fragments - having covalently attached
 PT non-proteinaceous polymer molecules, particularly polyethylene
 glycol, for improving the residence time in the circulation.
 PS Example K; Fig 41A-U; 328pp; English.
 CC This is the DNA sequence of vector plasmid p6g4v1ln35a.f(ab')2
 CC encoding a murine-human chimeric Fab (see W69313) containing
 CC complementarily determining regions of murine anti-interleukin-8
 CC (IL-8) monoclonal antibody (MAb) 6G5.2.5 (see W69309-10) in a
 CC human template. Humanised anti-IL-8 MAb (see W69301-04) are
 CC described for use in diagnostic applications and in the treatment
 CC of inflammatory disorders. The invention provides conjugates of an
 CC antibody fragment and a polymer, such as PEG, that have improved
 CC half-life, mean residence time, and/or clearance rate. The
 CC conjugates can be used for immune therapy of e.g. psoriasis,
 CC responses associated with inflammatory bowel disease (such as
 CC Crohn's disease and ulcerative colitis), ischemic reperfusion,
 CC adult respiratory distress syndrome, dermatitis, meningitis,
 CC encephalitis, uveitis, autoimmune diseases such as rheumatoid
 CC arthritis, Sjogren's syndrome, vasculitis, diseases involving
 CC leukocyte diapedesis, central nervous system inflammatory disorder,
 CC multiple organ injury syndrome secondary to septicemia or trauma,
 CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex
 CC mediated diseases, inflammations of the lung, including pleurisy,
 CC alveolitis, vasculitis, pneumonia, chronic bronchitis,
 CC bronchiectasis, and cystic fibrosis.
 SQ Sequence 6563 BP; 1537 A; 1790 C; 1675 G; 1561 T;

Query Match 65.1%; Score 488; DB 1; Length 6563;
 Best Local Similarity 79.4%; Pred. No. 3.2e-112;
 Matches 578; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 21 TCTCTCCTCTGCTAGTACGCGCGGCTCCCAAGTCCCAAGTCCGATCCGG 80
 DB 1281 TAGTTCGTTTCTTCTTCTGCTACAAACGCGTACGCTGAGTTACGTAAGTCTGG 1340
 QY 81 CCGCGAGGTCAAGAACGCGCGGCTCAGTCAAAAGTCTCTGTAAGCTAGCGCTATAT 140
 DB 1341 CGGTGCGCTGTGACGACGAGGGGCTCAGTCCGTTGCTGCTGACAGCTTGGCTATC 1400
 QY 141 TTTTCTATATATGATTGAATTAATGGTGGCTGACGCGCGGCAAGGCTCGAATGAT 200
 DB 1401 CTTCTGAGACACTATATGACATGGGTCGCGACGCGCGGCTGAAGGCTCGAATGAT 1460
 QY 201 GGGTGAATTTACCGGGGCTCTGTGACGCGATATACGCAAAATTTAAAGCCGCT 260
 DB 1461 TGGATTTATGATTCCTCCATAGGTGAACCTAGCTATATCAAAAGTTCAAGGGCGCTT 1520
 QY 261 TACTATGACGCTGACACTTGAAGTATGATGAGTCTGACGCTCGAGATC 320
 DB 1521 CATTTATCTCGGACACACTCCAAAACACACATCTGAGATGAACAGCTCGCGGC 1580
 QY 321 GGAGACACGCGCTTATATTTGGCGGCTTATTTTGGTCTTAGCCCGAATTTGTA 380
 DB 1581 TGAGGACACTGCGGTATATCTGCAAGAGGGGATTTATGCTACATGCTGATGCTT 1640

QY 381 TTTGATGTTTGGGTCAGGAACCTGTGCTCTGACGCGCTCCACCAAGGCGCC 440
 DB 1641 CTTCACGCTGTGGGTCAAGGAACCTGTGCTCTGCGGCTCCACCAAGGCGCC 1700
 QY 441 ATCGTCTTCCCTCTGGGCGCTCTCTCCAAAGACACCTTGGGGGACAGCGGCTTGG 500
 DB 1701 ATCGGTCTTCCCTCTGGGCGCTCTCTCCAAAGACACCTTGGGGGACAGCGGCTTGG 1760
 QY 501 CTGGCTGTGCAAGACTCTTCCCGAACCCTGTGAGGCTGTGGAATCAGGCGCCT 560
 DB 1761 CTGCTGTGCAAGACTCTTCCCGAACCCTGTGAGGCTGTGGAATCAGGCGCCT 1820
 QY 561 GACGACGCGGCTGACACCTTCCCGGCTGTCTTACAGTCTTCCAGACTTACTCCCTAG 620
 DB 1821 GACGACGCGGCTGACACCTTCCCGGCTGTCTTACAGTCTTCCAGACTTACTCCCTAG 1880
 QY 621 CAGCGTGTGACGCTGCTTCCCGGCTGTGAGGCAACCTACATCTGCAAGCTGA 680
 DB 1881 CAGCGTGTGACGCTGCTTCCCGGCTGTGAGGCAACCTACATCTGCAAGCTGA 1940
 QY 681 TCACAAAGCCGACACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGCAAAAC 740
 DB 1941 TCACAAAGCCGACACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGCAAAAC 2000
 QY 741 TCACACAT 748
 DB 2001 TCACACAT 2008

RESULT 11
 X06951
 ID X06951 standard; DNA; 1449 BP.
 AC X06951:
 DT 10-MAY-1999 (first entry)
 DE Monoclonal antibody 4B5 heavy chain variable region DNA.
 KW Antigen binding fragment 4B5; monoclonal antibody; cancer;
 KW neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
 KW sarcoma; lung carcinoma; metastasis; anti-idiotypic antibody;
 KW GD2 antigen; human; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 19..1449
 FT /*tag= a
 PN W09902545-A2.
 PD 21-JAN-1998.
 PE 08-JUL-1998; IB1046.
 PR 08-JUL-1997; US-051945.
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 PI Dan MD;
 DR WPI: 99-120769/10.
 P-PSDB: W88464.
 DT New antibody 4B5 polynucleotides and polypeptides - used to develop
 PT products for the diagnosis and treatment of cancers and for
 PT prophylactic therapy to reduce risk of recurrence
 PS Claim 3; Page 77-78; 83pp; English.
 CC This is the DNA sequence of a polynucleotide that encodes the heavy
 CC chain variable region (see W88464) of the recombinant human
 CC monoclonal antibody (MAb) 4B5. 4B5 recognises antibodies specific
 CC for GD2 antigen antibodies. Antibodies specific for GD2 recognise
 CC various cancers including glioblastoma, neuroblastoma, malignant
 CC and/or metastatic melanoma, breast adenocarcinoma, lung
 CC adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
 CC prostate adenocarcinoma. The invention encompasses 4B5 derivatives
 CC with immunologic specificity for antibodies specific for GD2. These
 CC derivatives, or antigen binding fragments, comprise regions of the
 CC 4B5 VDJ junction and regions spanning the 4B5 CDRs. Other
 CC derivatives include Fab, Fab', Fab', scv and isolated heavy and
 CC light chains. Polynucleotide fragments (see X06951-54), both
 CC coding and complementary strands, encoding 4B5 antibody V regions
 CC are also provided, as well as therapeutic plasmids and vectors,
 CC including vaccinia virus vectors, comprising these polynucleotides.
 CC 4B5 has been shown to mimic GD2, and is particularly useful in
 CC generating a host immune response to cancer. Products of the

CC invention can be used in the detection and treatment of e.g.
CC astrocytoma, oligodendroglioma, ependymoma, medulloblastoma,
CC primitive neural ectodermal tumour (PNET), pancreatic ductal
CC adenocarcinoma, small and large cell lung adenocarcinomas,
CC squamous cell carcinoma, bronchoalveolar carcinoma, epithelial
CC adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma,
CC breast tumours such as ductal and lobular adenocarcinoma, squamous
CC and adenocarcinomas of the uterine cervix, uterine and ovarian
CC epithelial carcinoma, prostatic adenocarcinoma, transitional
CC squamous cell carcinoma of the bladder, B and T cell lymphoma
CC (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
SQ Sequence 1449 BP; 342 A; 457 C; 398 G; 252 T;

Query Match 55.0%; Score 487.8; DB 1; Length 1449;
Best Local Similarity 78.8%; Pred. No. 2.4e-112;
Matches 601; Conservative 0; Mismatches 147; Indels 15; Gaps 1;
QY 1 ATGAAGTGGAGCTGGGTATTCTCTCTCTGTCAGTAACCTGCGGGGCTCCACCTCCCAA 60
DB 19 ATGGACTGGACCTGGAGGGTCTCTTTTGGTGGCAGCAGCTACAAGTGGCGGCTCCACG 78
QY 61 GTCCAACTGGTGCATCCGGCCGAGGTCAAGAAGCCAGGGGCTCAGTCAAAAGTGTCC 120
DB 79 GTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCTGGGGCTCAGTGAAGGTCTCC 138
QY 121 TGTAAAGCTAGCGCTATATTTTCTTAATTTATTTGGATTAATGGTGGTGCAGTGGTCC 180
DB 139 TGAAGGCTTCTGGATACACCTTCACCAAGTTTGTATCTCAACTGGTGGTGGAGCCCT 198
QY 181 GGCAGGCGCTGAATGGATGGTGGTGGATCTACCGGGCTCTGTAGCACCAGATATACC 240
DB 199 GGACAGGCTTGGTGGATGGGATGGATGAACCTTAACAGTGGTAAACAGGCTATGCA 258
QY 241 GAAATTTTAAAGACCTGTACTACGCGGTGACACTTCGACTAGTACAGTATACATG 300
DB 259 CAGAAGTTCCAGGCGAGTCAACCATGACACAGGAAACACTCCATAAGAAGACCTACATG 318
QY 301 GAGCTCTCAGCTGCATCGGAGGACAGCGCCGTCTATTATTTGGCGCGTTAT----- 354
DB 319 GAGCTGAGTGGCTGAGATCTGAGGACAGCGCCGTGATTTCTGTGCGGAAATGCCGAT 378
QY 355 -----TTTTTGGTCTTAGCCGGAATGGTATTTTGTATGTTGGGTGACAGGAC 405
DB 379 AAGCTAGAGATGGTGCATTTACACTACTACGGTATGGAGCGTGGGGCCAGGGACC 438
QY 406 CTGGTCACTCTCGAGCGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCGCCCTCC 465
DB 439 ACGTCACTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCTCC 498
QY 466 TCAAGAGCACTCTGGGGGACAGCGCCCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTG 525
DB 499 TCAAGAGCACTCTGGGGGACAGCGCCCTGGGTGCTGCTGCTGCTGCTGCTGCTGCT 558
QY 526 GAACCGTGTGCGTGTGGAACCTGAGGCGCCCTGACACGCGGCTGCACACCTTCCG 585
DB 559 GAACCGTGTGCGTGTGGAACCTGAGGCGCCCTGACACGCGGCTGCACACCTTCCG 618
QY 586 GCTGTCTCTACAGTCTCAGGACTCTACTCTCCTCAGCAGCGTGGTACCGTGCCTCCAGC 645
DB 619 GCTGTCTCTACAGTCTCAGGACTCTACTCTCCTCAGCAGCGTGGTACCGTGCCTCCAGC 678
QY 646 AGCTTGGGCACTCAGACCTTACATCTGCACTGATATCAAGAGCCAGCAACCAAGGTG 705
DB 679 AGCTTGGGCACTCAGACCTTACATCTGCACTGATATCAAGAGCCAGCAACCAAGGTG 738
QY 706 GACAAGAAAGTTGAGCCCAATCTTGTGACAAAACCTCACAT 748
DB 739 GACAAGAAAGTTGAGCCCAATCTTGTGACAAAACCTCACAT 781

RESULT 12

X06952/c
ID X06952 standard; DNA; 1449 BP.
AC X06952;
DT 10-MAY-1999 (first entry)
DE Monoclonal antibody 4B5 heavy chain variable region DNA.
KW Antigen binding fragment 4B5; monoclonal antibody; cancer;
KW neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
KW sarcoma; lung carcinoma; metastasis; anti-idiotypic antibody;
KW CD2 antigen; human; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS complement (1..1431)
FT /*tag= a
PN W09902545-A2.
PD 21-JAN-1999.
PF 08-JUL-1998; IB1046.
PR 08-JUL-1997; US-051945.
PA (NOVO-) NOVOPHARM BIOTECH INC.
PI Dan MD;
DR WPI; 99-120769/10.
DR P-PSDB; W88464.
PT New antibody 4B5 polynucleotides and polypeptides - used to develop
PT products for the diagnosis and treatment of cancers and for
PT prophylactic therapy to reduce risk of recurrence
PS Claim 6; Page 78; 83pp; English.
CC This is the complementary strand of a DNA sequence (see also
CC X06951) that encodes the heavy chain variable region (see W88464)
CC of the recombinant human monoclonal antibody (MAB) 4B5. 4B5
CC recognises antibodies specific for GD2 antigen antibodies. Such
CC antibodies recognise various cancers including glioblastoma,
CC neuroblastoma, malignant and/or metastatic melanoma, breast
CC adenocarcinoma, lung adenocarcinoma, small cell lung carcinoma,
CC colon adenocarcinoma and prostate adenocarcinoma. The invention
CC encompasses 4B5 derivatives with immunologic specificity for
CC antibodies specific for GD2. These derivatives, or antigen binding
CC fragments, may comprise regions of the 4B5 VDJ junction and regions
CC spanning the 4B5 CDRs. Other derivatives include Fab, Fab'/2,
CC Fab', scFv and isolated heavy and light chains. Polynucleotide
CC fragments (see X06951-54), both coding and complementary strands,
CC encoding 4B5 antibody V regions are also provided, as well as
CC therapeutic plasmids and vectors, including vaccinia virus vectors,
CC comprising these polynucleotides. 4B5 mimics GD2, and is useful in
CC generating a host immune response to cancer. Products of the
CC invention can be used in the detection and treatment of e.g.
CC astrocytoma, oligodendroglioma, ependymoma, medulloblastoma,
CC primitive neural ectodermal tumour (PNET), pancreatic ductal
CC adenocarcinoma, small and large cell lung adenocarcinomas,
CC squamous cell carcinoma, bronchoalveolar carcinoma, epithelial
CC adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma,
CC breast tumours such as ductal and lobular adenocarcinoma, squamous
CC and adenocarcinomas of the uterine cervix, uterine and ovarian
CC epithelial carcinoma, prostatic adenocarcinoma, transitional
CC squamous cell carcinoma of the bladder, B and T cell lymphoma
CC (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
SQ Sequence 1449 BP; 252 A; 398 C; 457 G; 342 T;

Query Match 55.0%; Score 487.8; DB 1; Length 1449;
Best Local Similarity 78.8%; Pred. No. 2.4e-112;
Matches 601; Conservative 0; Mismatches 147; Indels 15; Gaps 1;

QY 1 ATGAAGTGGAGCTGGGTATTCTCTCTCTGTCAGTAACCTGCGGGGCTCCACCTCCCAA 60
DB 1431 ATGGACTGGACCTGGAGGGTCTCTTTTGGTGGCAGCAGCTACAAGTGGCGGCTCCACG 1372
QY 61 GTCCAACTGGTGCATCCGGCCGAGGTCAAGAAGCCAGGGGCTCAGTCAAAAGTGTCC 120
DB 1371 GTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCTGGGGGCTCAGTGAAGGTCTCC 1312
QY 121 TGTAAAGCTAGCGCTATATTTTCTTAATTTATTTGGATTAATGGTGGTGGTGGTGGTGG 180
DB 1311 TGCAGGCTTCTGGATACACCTTCACCTTCACAGTTTGTATCTCAACTGGTGGTGGTGGTGG 1252


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QY 355 -----TTTTTGGTTCTAGCCGAAATGGTATTGTTTGGGTCAAGGAACC 405
Db 395 AGCAGGCAATTTGACCGGGCCGGTGGCTGGTTCGACCCCTGGGGCCAGGCACC 454
QY 406 CTGGTCACTCTCTGAGCGCTCCACCAAGGGCCCATCGGCTTCCTCCCTGGCCCTCC 465
Db 455 CTGGTCACTCTCTCTGAGCGCTCCACCAAGGGCCCATCGGCTTCCTCCCTGGCCCTCC 514
QY 466 TCCAAGAGCACCCTGGGGGCACAGCGCCCTGGCTGGCTGGTCAAGGACTACTTCCC 525
Db 515 TCCAAGAGCACCCTGGGGGCACAGCGCCCTGGCTGGCTGGTCAAGGACTACTTCCC 574
QY 526 GAACCGGTGACGGTGTGGTGAAGCTCAGGCGCCCTGACACGCGGTGCACACCTTCCCG 585
Db 575 GAACCGGTGACGGTGTGGTGAAGCTCAGGCGCCCTGACACGCGGTGCACACCTTCCCG 634
QY 586 GCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTCAAGGCTCCAGC 645
Db 635 GCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTCAAGGCTCCAGC 694
QY 646 AGCTTGGGCACCCAGACCTACATCTCAAGCTGAATCACAAGCCAGCAACCAAGGTG 705
Db 695 AGCTTGGGCACCCAGACCTACATCTCAAGCTGAATCACAAGCCAGCAACCAAGGTG 754
QY 706 GACAAGAAAGTTGAGCCCAAAATCTGTGACAAAATCTACACAT 748
Db 755 GACAAGAAAGTTGAGCCCAAAATCTGTGACAAAATCTACACAT 797
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RESULT 14

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Q65629
ID Q65629 standard; DNA; 9208 BP.
AC Q65629;
DT 01-FEB-1995 (first entry)
DE Vector contg. TCAE 8 DNA.
KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
OS Synthetic; ss.
PN W09411026-A.
PD 26-MAY-1994.
PF 12-NOV-1993; U10953.
PR 13-NOV-1992; US-978891.
PR 03-NOV-1993; US-149099.
PA (IDEC-) IDEC PHARM CORP.
PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;
PI Refine;
DR WPI; 94-183162/22.
PT Treating B cell lymphoma with chimeric antibody - against CD20,
PT causing rapid depletion of peripheral B cells, also new
PT antibodies and hybridomas
PS Disclosure; Fig 3; 101pp; English.
CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric
CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8
CC contains 4 transcriptional cassettes, human Ig light and heavy chain
CC constant regions, dihydrofolate reductase, neomycin phosphotransferase
CC and murine variable regions. The vector can be used to produce
CC antibodies which cause depletion of peripheral blood B cells,
CC including those associated with lymphoma. They mediate complement-
CC dependent lysis and lyse target cells by antibody-dependent cellular
CC cytotoxicity.
CC See also Q65629-35.
SQ Sequence 9208 BP; 2237 A; 2399 C; 2388 G; 2182 T;
```

```
Query Match 63.5%; Score 476; DB 1; Length 9208;
Best Local Similarity 78.2%; Pred. No. 3.3e-109;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;
QY 1 ATGAAGTGGAGCTGGGTATTCTCTTCTCTGTCAGTAACTGCGGCGTCCACATCCCAA 60
Db 2400 ATGGGTTGGAGCCCTCATCTTCTCTCTCTGTCGTGTCATCGCTGTCCTGCCAG 2459
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QY 61 GTCCAACCTGGTCAATCGGCGCCGAGGTCAAGAAAGCCAGGGCCCTCAGTCAAAGTGTC 120
Db 2460 GTACAACCTGCAGCACCCCTGGGCTGAGCTGGTGAAGCCCTGGGGCCCTCAGTGAAGTGTC 2519
QY 121 TGTAAAGCTAGCGGCTATATTTTTTCTTAATTATTGGAATTCATATGGGTGGGTGAGGCC 180
Db 2520 TGTAAAGCTAGCGGCTATATTTTTTCTTAATTATTGGAATTCATATGGGTGGGTGAGGCC 2579
QY 181 GGGCAGGCGCTGGGAATGGATGGTGGATCTTACCGGCTCTGGTAGCACCCGAATATACC 240
Db 2580 GGTGGGCGCTGGGAATGGATGGAGCTATTATCCCGAAATGGTGAATCTTCCACAAAT 2639
QY 241 GAAATTTTAAAGACCGCTGTACTATGACGCGTGCACACTTCGACTAGTACAGTATACATG 300
Db 2640 CAGAGTTCAAGGCAAGGCCACATGACTGCAGACAAATCTCCAGCACACCTACATG 2699
QY 301 GAGCTCTCCAGCCTCGGATCGGAGGACAGCGCCGCTCTATTATTGGCGCGGTATTATTTT 360
Db 2700 CAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGCTCTATTACTGTCAAGATCGACT-- 2757
QY 361 GGTCTAGCCGCAATTTGGTATTATTTTGGGTCTAAGGAACTCTGGTCACTGTCTCG 420
Db 2758 -ACTAGGCGGTGACTGGTACTTCAATGTCTGGGCGGAGGACACACGCTCACCGTCT 2816
QY 421 AGCGCTCTCCACCAAGGGCCATCGGTCTTCCCGCTGGGCGCCCTCTCCCAAGAGCACCTCT 480
Db 2817 CGAGTAGCACCAAGGGCCATCGGTCTTCCCGCTGGACCCCTCTCCCAAGAGCACCTCT 2876
QY 481 GGGGCGCAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGAGGTTG 540
Db 2877 GGGGCGCAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGAGGTTG 2936
QY 541 TCGTGAACCTAGGCGCCCTGACACGCGCGTGCACACCTTCCCGCTCTCTACAGTCC 600
Db 2937 TCGTGAACCTAGGCGCCCTGACACGCGCGTGCACACCTTCCCGCTCTCTACAGTCC 2996
QY 601 TCAGGACTCTACTCTCCTCAGCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660
Db 2997 TCAGGACTCTACTCTCCTCAGCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3056
QY 661 ACCTACATCTGCAAGCTGAATCACAAGCCGACCAACACCAAGTGGGACAAAGTTGAG 720
Db 3057 ACCTACATCTGCAAGCTGAATCACAAGCCGACCAACACCAAGTGGGACAAAGTTGAG 3116
QY 721 CCCAAATCTTGTGACAAAATCTACACAT 748
Db 3117 CCCAAATCTTGTGACAAAATCTACACAT 3144
```

RESULT 15

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V61793
ID V61793 standard; DNA; 19001 BP.
AC V61793;
DT 07-JUN-1999 (first entry)
DE Traget plasmid Molly containing anti-CD20 gene.
KW Molly; target plasmid; gene integration; gene amplification;
KW homologous recombination; vector; neomycin phosphotransferase;
KW neo gene; selectable marker; immunoglobulin; CD20; C2B8; human; ss.
OS Chimeric - Mus sp.
OS Chimeric - Escherichia coli.
OS Chimeric - Baculovirus.
OS Chimeric - Cytomegalovirus.
OS Chimeric - Rhesus macaque polyoma virus.
OS Chimeric - Photinus sp.
OS Chimeric - Salmonella typhimurium.
OS Chimeric - Homo sapiens.
FH Key Location/Qualifiers
FT misc_feature 361..363
FT /tag= a
FT /note= *these bases represent nucleotides missing
FT from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
```


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a

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GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 20:37:50 ; Search time 56.72 Seconds

(without alignments)
1818.880 Million cell updates/sec

Title: US-08-487-283a-12

Perfect score: 750
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24380 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
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3: /cgnl_7/prodata/1/ina/5C_COMB.seq: *
4: /cgnl_7/prodata/1/ina/5D_COMB.seq: *
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7: /cgnl_7/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495.2	66.0	8120	5 US-09-027-449-68	Sequence 68, Appl
2	488	65.1	800	5 US-09-027-449-69	Sequence 69, Appl
3	488	65.1	927	5 US-09-027-449-59	Sequence 59, Appl
4	488	65.1	6563	5 US-09-027-449-61	Sequence 61, Appl
5	478.2	63.8	1617	3 US-08-378-939-9	Sequence 9, Appl
6	476	63.5	9209	2 US-08-149-099C-3	Sequence 3, Appl
7	476	63.5	9209	2 US-08-476-275-2	Sequence 2, Appl
8	476	63.5	9209	3 US-08-478-967A-3	Sequence 3, Appl
9	476	63.5	18986	3 US-08-819-866-2	Sequence 2, Appl
10	476	63.5	18986	4 US-09-023-715-2	Sequence 2, Appl
11	467.4	62.3	3282	1 US-08-276-852-154	Sequence 154, App
12	467.4	62.3	3282	1 US-08-276-852-169	Sequence 169, App
13	467.4	62.3	3282	2 US-08-899-575-154	Sequence 154, App
14	467.4	62.3	3282	2 US-08-899-575-169	Sequence 169, App
15	467.4	62.3	3282	2 US-08-899-575-154	Sequence 154, App
16	467.4	62.3	3282	2 US-08-899-575-169	Sequence 169, App
17	467.4	62.3	3282	6 PCT-US95-08743-154	Sequence 154, App
18	467.4	62.3	3282	6 PCT-US95-08743-169	Sequence 169, App
19	467.4	62.3	13254	1 US-08-276-852-156	Sequence 156, App
20	467.4	62.3	13254	2 US-08-276-852-170	Sequence 170, App
21	467.4	62.3	13254	2 US-08-899-575-156	Sequence 156, App
22	467.4	62.3	13254	2 US-08-899-575-170	Sequence 170, App
23	467.4	62.3	13254	2 US-08-899-575-156	Sequence 156, App
24	467.4	62.3	13254	2 US-08-899-575-170	Sequence 170, App
25	467.4	62.3	13254	6 PCT-US95-08743-156	Sequence 156, App
26	467.4	62.3	13254	6 PCT-US95-08743-170	Sequence 170, App

27	459.6	61.3	762	1 US-08-398-613A-57	Sequence 57, Appl
28	459.6	61.3	762	2 US-08-398-612A-57	Sequence 57, Appl
29	459.6	61.3	762	1 US-08-398-611A-57	Sequence 57, Appl
30	459.6	61.3	762	2 US-08-398-611A-57	Sequence 57, Appl
31	459.6	61.3	762	3 US-08-491-334A-57	Sequence 57, Appl
32	459.6	61.3	762	5 US-09-027-449-43	Sequence 43, Appl
33	453.8	60.5	2178	2 US-08-463-587A-24	Sequence 24, Appl
34	453.8	60.5	2178	3 US-08-463-587A-2	Sequence 2, Appl
35	453.8	60.5	2178	5 US-08-923-854-24	Sequence 24, Appl
36	453.8	60.5	2178	6 PCT-US91-09133-25	Sequence 25, Appl
37	443.2	59.1	687	1 US-08-300-386A-1	Sequence 1, Appl
38	443.2	59.1	687	6 PCT-US94-01258-1	Sequence 1, Appl
39	443.2	59.1	687	6 PCT-US95-11235-1	Sequence 1, Appl
40	442.2	59.0	6557	1 US-08-286-740-3	Sequence 3, Appl
41	442.2	59.0	6557	6 PCT-US95-09576-3	Sequence 3, Appl
42	434.4	57.9	11528	5 US-08-444-644-18	Sequence 18, Appl
43	432.8	57.7	756	1 US-08-398-613A-29	Sequence 29, Appl
44	432.8	57.7	756	1 US-08-398-612A-29	Sequence 29, Appl
45	432.8	57.7	756	2 US-08-398-611A-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-027-449-68
Sequence 68, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatln (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P108583-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 8120 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-027-449-68


```

QY 61 GTCCACTGTCATCCGCGCCGAGGTCAAGAGCCAGGGGCTCAGTCAAAAGTCTCC 120
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Db 95 ATGAGGTGGTGAAGTCTGGGGCTGAAGTAAGAGAGCTGGGTCTCGTGACGGTCTCC 154
   || || || || || || || || || || || || || || || || || || || ||
QY 121 TGTAACTAGCGGCTATATTTTCTATATTGATTCATGGGTGCTGAGGCCCC 180
   || || || || || || || || || || || || || || || || || || || ||
Db 155 TGCAAGCATCTGAGAGCCTTACGAACATATGTATCAGTGGGTCTGAGAGCCCT 214
   || || || || || || || || || || || || || || || || || || || ||
QY 181 GGGGAGGCGCTGATGGATGGGTGATCTTACCGGCTCTGAGAGACCGAAATATACC 240
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Db 215 GGAACAGGCTTGATGGATGGAGGATCATCCCTTTTGGTACCAACCACTACTCA 274
   || || || || || || || || || || || || || || || || || || || ||
QY 241 GAAATTTTAAAGACCGTGTACTATGACGGGTGACACTGACAGTATGATATATG 300
   || || || || || || || || || || || || || || || || || || || ||
Db 275 CAGACTTCCAGGGGAGAGTACACATTACCGCGAATCCACAGACAGCCACATG 334
   || || || || || || || || || || || || || || || || || || || ||
QY 301 GAGCTCTCCAGCGCTGCATCGAGACACAGGCGCTATATATGCGCGCTTAT- 354
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Db 335 GAGCTGACTAGCCTGAGATCTGAGGACACAGGCGCTGATCTGATGCGACAGATCGTAC 394
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QY 355 -----TTTTTGGTTCAGCCCGAATTGATTTTGTATGTTGGGGTCAAGAAC 405
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Db 395 AGCGAGGCAATTTTGGACCGGGCGGCTGCTGATTCGACCCCTGGGGCCAGGGCAC 454
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QY 406 CTGGTCACTGCTCGAGCGCTCCACCAAGGGCCCATGCTTCCCTGGCGGCTTCC 465
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Db 455 CTGGTCACTGCTCTCTCAGCTCCACCAAGGGCCCATGCTTCCCTGGCGGCTTCC 514
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QY 466 TCCAGAGCACCTCTGGGGGACACAGCGGCTGGGCTGCTGCTCAGAGACTTCTCC 525
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Db 515 TCCAGAGCACCTCTGGGGGACACAGCGGCTGGGCTGCTGCTCAGAGACTTCTCC 574
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QY 526 GAACCGGTGACGGTGTGTGGAATCAGGGCCCTGACAGCGGGGTGACACCTTCC 585
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Db 575 GAACCGGTGACGGTGTGTGGAATCAGGGCCCTGACAGCGGGGTGACACCTTCC 634
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QY 586 GGTGTCTAGTCTGCTGAGACTCTACTCCCTCAGACAGCGGTGAGCGGCTCCAGC 645
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Db 635 GGTGTCTAGTCTGCTGAGACTCTACTCCCTCAGACAGCGGTGAGCGGCTCCAGC 694
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QY 646 AGCTTGGGACCCAGACTACATCTGCAACGTGATCAACAGCCAGCAACCAAGGTG 705
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Db 695 AGCTTGGGACCCAGACTACATCTGCAACGTGATCAACAGCCAGCAACCAAGGTG 754
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QY 706 GACAGAAAGTTGAGCCCAATCTTGTGACAAACTACACAT 748
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Db 755 GACAAAGAAAGTTGAGCCCAATCTTGTGACAAACTACACAT 797
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,099C
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 12-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9209 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
;
US-08-149-099C-3
;
Query Match 63.5%; Score 476; DB 2; Length 9209;
Best Local Similarity 78.2%; Pred. No. 5,9e-115;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;
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QY 1 ATGAATGAGAGTGGTGGTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
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Db 2401 ATGGGTGAGAGCTTATCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
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QY 61 GTCCACTGTCATCCGCGCCGAGGTCAAGAGCCAGGGGCTCAGTCAAAAGTCTCC 120
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Db 2461 GATCAACTGACAGCTGAGGCTGAGTGTGAAAGCTGGGGCTCAGAGAGATGTCC 2520
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QY 121 TGTAAAGTCAAGGGCGTATTTTCTATATTGATTCATGGGTGCTGAGGCCCC 180
   || || || || || || || || || || || || || || || || || || || ||
Db 2521 TCCAAAGCTTGTGCTACATTTACATTAATATGACAGTGAATTAACAGACACT 2580
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QY 181 GGGCAGGCGCTGAAATGATGGGTGAGATCTTACCGGGCTCTGAGACCGAATATAC 240
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Db 2581 GGTGGGGCTTGAATGATTTGAGATTTATCCCGGAATGATGATCTTCTCAAT 2640
   || || || || || || || || || || || || || || || || || || || ||
QY 241 GAAATTTTAAAGACCGTGTACTATGACCGGTGACACTTGCATGATGATGATGATG 300
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Db 2641 CAGAAATTAAGAGCAAGGCAAGCATGATGACAGCAAAATCCACAGCAGCTACATG 2700
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QY 301 GAGCTCTCAGCGCTGATCGAGAGACAGGCGCTATATTATTTGCGCGCTATTTT 360
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Db 2701 CAGCTCAGAGCTGACATCTGAGACTCTGCGGTATATTACTGTCAAGATGACTT 2758
   || || || || || || || || || || || || || || || || || || || ||
QY 361 GGTCTAGCCCGAATGATTTTGTGTTGGGGTCAAGGAACCGTGGTCACTGCTCG 420
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Db 2759 -ACTACGGGGGTGATCTGATCTTCAATGTCTGGGGGACAGGACACAGGCTGCT 2817
   || || || || || || || || || || || || || || || || || || || ||
QY 421 AGCGCTCCACCAAGGGCCCATCGTCTTCCCGCTGGCGCTCTCTCAAGAGCAGCTCT 480
   || || || || || || || || || || || || || || || || || || || ||
Db 2818 GCAGTACAGCAACAGGGCCCATCGTCTTCCCGCTGGACCGCTCTCAAGAGCAGCTCT 2877
   || || || || || || || || || || || || || || || || || || || ||
QY 481 GGGGACACAGGCGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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Db 2878 GGGGGACACAGGCGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2937
   || || || || || || || || || || || || || || || || || || || ||
QY 541 TGTGGAATCAAGGCGCTGACACAGGCGGTGACACACTTCCCGGCTGCTCAAGCTCC 600
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Db 2938 TCAGTGAACCTCAGCGCCCTGACACAGCGCGTGCACACATCTCCGGCTGTCTCTACAGTCC 2997
QY 601 TCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAG 660
Db 2998 TCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAG 3057
QY 661 ACCTACATCTGCAACGTGAATCACAAGCCCGCAGCAACACCAAGGTTGGCAAGAAAGTTGAG 720
Db 3058 ACCTACATCTGCAACGTGAATCACAAGCCCGCAGCAACACCAAGGTTGGCAAGAAAGTTGAG 3117
QY 721 CCCAAATCTGTGACAAAACCTCACACAT 748
Db 3118 CCCAAATCTGTGACAAAACCTCACACAT 3145

RESULT 7

US-08-476-275-2
; Sequence 2, Application US/08476275
; Patent No. 5776456
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/476,275
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9209 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: anti-CD20 in TCAE 8
US-08-476-275-2

Query Match 63.5%; Score 476; DB 2: Length 9209;
Best Local Similarity 78.2%; Pred. No. 5.9e-115;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;
QY 1 ATGAAGTGGAGCTGGGTTATTCTTCTCTCTGTCTCAGTAACCTCCGGCGCTCCACATCCCAA 60
Db 2401 ATGGGTTGGAGCCTCATCTTGCTCTTCTTGTGCTGTTGTGTCTCTCTCTCTCTCTCTCCAG 2460
QY 61 GTTCAACTGGTGCATCCGGCCCGCAGGTCAAGAGCCAGGCGGCTCAGTCAAAAGTGTCC 120
Db 2461 GTTCAACTGGAGCCTGGGCTGAGCTGTAAGCCCTGGGCGCTCAGTGAAGATGTCC 2520
QY 121 TGTAAAGCTAGCGCTATATTTTCTAATTTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTT 180
Db 2521 TGTAAAGCTAGCGCTATATTTTCTAATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTT 2580
QY 181 GGGCAGGCGCTGGAATGGATGGTGGATGAGATCTTACCGGGCTCTGGTAGCAGCCGAATATACC 240
Db 2581 GGTGCGGCGCTGGAATGGATGGAGCTATTTATCCGGAAATGGTATCTTCTTCTTCTTCTTCT 2640
QY 241 GAAATTTTAAAGACCGTGTACTATGAGCGTGCACACTTCGACTAGTACAGTATACATG 300
Db 2641 CAGAAAGTTCAAAAGCAAGGCCACATTGACTGCAGACAAATCTCCAGCAGCAGCTACATG 2700
QY 301 GAGCTCTCCAGCCTCGGATCGGAGCAGCGCGCTCTATTATTGCGCGGTTATTTTTT 360
Db 2701 CAGCTCAGCAGCCTGACATCTGAGGACTCTCGGGTCTATTACTGTGCAAGATCGAGTT-- 2758
QY 361 GTTCTAGCCCCAAATTTGTTATTTTGGGTTTGGGTTCAAGGAACCTTGGTCACTGTCTCG 420
Db 2759 -ACTAGCGGCTGACTGGTACTTCAATGTCTGGGCGCAGGACACGCTCACCCTCTCT 2817
QY 421 AGCGCTCTCACAAGGCGCCATCGGTCTTCCCGCTGGCGCCCTCTCTTCCAGAGCAGCTCT 480
Db 2818 GCAGCTAGCACCAGGCGCCATCGGTCTTCCCGCTGGCACCCTCTCTTCCAGAGCAGCTCT 2877
QY 481 GGGGCGCAGCGCGCCCTGGGCTGCGCTGCTCAAGGACTACTTCCCGAACCCGTTGACGGTG 540
Db 2878 GGGGCGCAGCGCGCCCTGGGCTGCGCTGCTCAAGGACTACTTCCCGAACCCGTTGACGGTG 2937
QY 541 TCGTGAACCTCAGCGCCCTGACACGCGCGTGCACACCTTCCCGCTGCTCTCTACAGTCC 600
Db 2938 TCGTGAACCTCAGCGCCCTGACACGCGCGTGCACACCTTCCCGCTGCTCTCTACAGTCC 2997
QY 601 TCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGTGACCGTGTGACCGTGTGACCGTGTG 660
Db 2998 TCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGTGACCGTGTGACCGTGTGACCGTGTG 3057
QY 661 ACCTACATCTGCAAGCTGAATCACAAGCCCGCAGCAACACCAAGTGGCAAGAAAGTTGAG 720
Db 3058 ACCTACATCTGCAAGCTGAATCACAAGCCCGCAGCAACACCAAGTGGCAAGAAAGTTGAG 3117
QY 721 CCCAAATCTGTGACAAAACCTCACACAT 748
Db 3118 CCCAAATCTGTGACAAAACCTCACACAT 3145

RESULT 8

US-08-478-967A-3
; Sequence 3, Application US/08478967A
; Patent No. 5843439
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; APPLICANT: HANNA, Nabil
; APPLICANT: LEONARD, John E.
; APPLICANT: NEWMAN, Roland A.
; APPLICANT: REFF, Mitchell E.
; APPLICANT: RASTETTER, William H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIO-LABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; TITLE OF INVENTION: LYMPHOMA

```

1 NUMBER OF SEQUENCES: 9
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
4 STREET: P.O. Box 1404
5 CITY: Alexandria
6 STATE: Virginia
7 COUNTRY: United States
8 ZIP: 22113-1404
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/478,967A
17 FILING DATE:
18 CLASSIFICATION: 424
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/149,099
21 FILING DATE: 03-NOV-1993
22 APPLICATION NUMBER: US 07/978,891
23 FILING DATE: 12-NOV-1992
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Teskin, Robin L.
26 REGISTRATION NUMBER: 35,030
27 REFERENCE/DOCKET NUMBER: 012712-014
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (703) 836-6620
30 TELEFAX: (703) 836-2021
31 INFORMATION FOR SEQ ID NO: 3:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 9209 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: circular
37 MOLECULE TYPE: DNA (genomic)
38 HYPOTHETICAL: NO
39 ANTI-SENSE: NO
40
41 US-08-478-967A-3

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[illegible]

Oy	421	AGCGCTTCACACCAAGGGCCCATCGTGTTCCTCCCTGGGCGCTTCCTCAAGAGCAACTCT	480
Db	2818	GCAGCTACACCAAGGGCCCATCGTGTTCCTCCCTGGACACTCTCTCTCAAGACACTCT	2877
Oy	481	GGGGGCACAGCGGCGCTGTGGGCTGCTGTGTCAAAGACTACTTCCCGCAACCGGTGACGGTG	540
Db	2878	GGGGGCACAGCGGCGCTGTGGGCTGCTGTGTCAAAGACTACTTCCCGCAACCGGTGACGGTG	2933
Oy	541	TCGTGGAACTCAGGCGGCGCTGTGACCAAGCGGGGTGCACACCTTCCCGGCTGTCTAAGTCC	600
Db	2938	TCGTGGAACTCAGGCGGCGCTGTGACCAAGCGGGGTGCACACCTTCCCGGCTGTCTAAGTCC	2997
Oy	601	TCAGGACTCTACTCCCTTCAGACAGCGTGTGTACCGTGCCTCCAGCAAGCTTTGGGCAACCA	660
Db	2998	TCAGGACTCTACTCCCTTCAGACAGCGTGTGTGTACCGTGCCTCCAGCAAGCTTTGGGCAACCA	3057
Oy	661	ACCTACACTCTGCAACGGTAATCAACAACCCAGAACCAACCAAGGTGGACAAAGAAAGTTGAG	720
Db	3058	ACCTACACTCTGCAACGGTAATCAACAACCCAGAACCAACCAAGGTGGACAAAGAAAGCGAG	3117
Oy	721	CCCAATCTGTGTGACAAAGACTCAACACT	748
Db	3118	CCCAATCTGTGTGACAAAGACTCAACACT	3145

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RESULT 9
US-08-819-866-2
: Sequence 2, Application US/08819866
: Patent No. 5830698
: GENERAL INFORMATION:
: APPLICANT: REEF, Mitchell E.
: APPLICANT: BARNETT, Richard Spence
: APPLICANT: MCILCHLAN, Karen Retta
: TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
: TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
: NUMBER OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/819,866
: FILING DATE: 14-MAR-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Teskin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-352
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18986 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-819-866-2

Query Match      63.5%      Score 476; DB 3; Length 18986;
Best Local Similarity 78.2%; Pred. No. 7,3e-115;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

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Best Local Similarity 78.7%: Pred. No. 7.5e-113;
Matches 577, Conservative 0; Mismatches 141; Indels 15; Gaps 1

OY      1 ATGAAGTGGAGCTGGGTTATTCTTCCTCCCTGTGATACATGCGGGCTCCACTGCCAA 60
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Db      15 ATGGAATGAGCTGGGTCTTCTCTCTCTCCTGTGATACATGAGGTGTCCACTGCCAG 74
OY      61 GTCCAACTGGTGCATATCCGGGGCGGAGGCAAGAAGCCGAGGGGCGCTCATCAAAGTCC 120
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Db      75 GTTCACTGGTGTTCACTCCGGGGCTAAGGTAAGAAAGCCGGGGCGCTCATGAAGTTTCT 134
OY      121 TGTAAAGCTAGCGGCTATATTTTCTTAATTAATTAATTAATTAATTAATTAATTAAT 180
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Db      135 TGTCAGGCTTCTCGATACAGATTCAAGTAACCTTGTATTCACTTGGGTGGCCAGCCCC 194
OY      181 GGGCAGGGCCCTGGAATGATGGGTAGATCTTACC GGCGCTGTGTAGCACCGAATATACC 240
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Db      195 GGACAGAGGTTTGAATGGATGGATGAGATCATCACTTACACAGGAACAAGAAATTTTCA 254
OY      241 GAATAATTTAAAGACCGGTACTATAGACCGCTGACACTGTGACATAGTACATATPACG 300
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Db      255 GCGAAGTTCAGAGAACAGATGCACCTTTACCCGGGACACATCCGCGAACAACCTACARG 314
OY      301 GAGCTCTCCAGCCTCGAATCGGAGACACAGCGCGCTATATTATTTGGCGC----- 348
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Db      315 GAGTTGAGGAGGCTTAGGCTGCAACACAGCGCTGTTTATTATTGTGCGAGATGGGGCCA 374
OY      349 ---CGTTATTTTTTGGTTCTAGCCCGAATGGAATTTTGTATGTTTGGGGTCAAGAMCC 405
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Db      375 TATAGTTGGATGATTTCTCCCAGAGACAATTAATATAGAGAGCTCGGGGGCAAGGAMCC 434
OY      406 CTGTGCTATGTCGACAGCGCCCTCCACCAAGGGCCCATGGTTCCTCCCTGGCGCCCTCC 465
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Db      435 ACGGTCATCTGAGCTCAGCTTCACCAAGGGCCCATGGTTCCTCCCTGGCACCTCC 494
OY      466 TCCAAGACCACTCTGGGGGGCACAGCGGCGCTGGGCTGCTGAAGGACTACTTCCC 525
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      495 TCCAAGACCACTCTGGGGGGCACAGCGGCGCTGGGCTGCTGTCGAAGGACTACTTCCC 554
OY      526 GAACCGGTGAGCGGTGCTGTAAGTCAAGGCGCGCTGACACAGCGGGGTGCACACTTCCG 585
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      555 GAACCGGTGAGCGGTGCTGTAAGTCAAGGCGCGCTGACACAGCGGGGTGCACACTTCCG 614
OY      586 GCTGTCTCAAGTCTCAAGACTCTACTCCCTCAGACAGCGGTGAGCGGTGCCCTCCAC 645
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Db      615 GCTGTCTCAAGTCTCTCAGACTCTACTCCCTCAGACAGCGGTGAGCGGTGCCCTCCAC 674
OY      646 AGCTTGGGCACCCAGACTTACATCTGCAACGTGATTCACAAACCCAGCAACCAAGGTG 705
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Db      675 AGCTTGGGCACCCAGACTTACATCTGCAACGTGATTCACAAACCCAGCAACCAAGGTG 734
OY      706 GACAAGAAAGTTG 718
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Db      735 GACAAGAAAGTTG 747

RESULT 14
US-08-899-575-169/c
: Sequence 169, Application US/08899575
: Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Bardas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mall Drop #PC8
CITY: La Jolla

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STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 3282 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IS-08-899-575-169

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Query Match	62.38;	Score 467.4;	DB 2;	Length 3282;
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[illegible]

5/7/18 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06105444 BIOSIS NO.: 000085068593
PREPARATION AND CHARACTERIZATION OF MONOCLONAL ANTIBODIES AGAINST THE FIFTH
COMPONENT OF RABBIT COMPLEMENT C5
AUTHOR: GICLAS P C; BAKER S L; GILLESPIE M L; WILCOX C
AUTHOR ADDRESS: DEP. PEDIATR., NATL. JEW. CENT. IMMUNOL. RESPIR. MED., 1400
JACKSON ST., DENVER, COLO. 80206, USA.
JOURNAL: J IMMUNOL METHODS 105 (2). 1987. 201-210.
FULL JOURNAL NAME: Journal of Immunological Methods
CODEN: JIMMB
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: By immunizing mice genetically deficient in C5 we were able to obtain a group of monoclonal antibodies to rabbit C5 that cross-react with C5 from a wide variety of mammalian sera, including mouse. The specificity of the monoclonal **antibodies** was against native C5 and C5b but not C5a. The **antibodies** strongly inhibit the expression of C5 hemolytic activity. We suggest that these monoclonal **antibodies** will be useful for studying C5 as well as providing a way to selectively deplete C5 from plasma in vitro or in vivo.